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                    Copyright
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- protein search, using sw model OM protein May 25, 2006, 14:52:22 ; Search time 196 Seconds Run on:

(without alignments)
335.914 Million cell updates/sec

US-10-614-481-9

759 1 MWLQNLLLLGTVVYSMPAPT......KNLKDFLFEIPFDCWKPAQK 144 Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2589679 segs, 457216429 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A\_Geneseq\_8:\*

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2003bs:\* geneseqp2003as:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:\*

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Result No.	Score	Query	Query Match Length	BO	QI	Description
-	759	100.0	144	4	ABP98711	Abp98711 Equine gr
7	759	100.0	144	4	AAB37147	7 Equine
m	641	84.5	144	~	AAR23662	
4	587	77.3	144	~	AAR54818	8
ß	586	77.2	144	Н	AAP60418	Aap60418 Human gra
φ	286	77.2	144	7	AAP70657	Aap70657 Sequence
7	586	77.2	144	~	AAR04098	8
60	586	77.2	144	~	AAR71118	
σ	586	77.2	144	~	AAR92800	Aar92800 Human GM-
10	586	77.2	144	~	AAW60031	Aaw60031 Human gra
11	586	77.2	144	m	AAB18633	Aab18633 Amino aci
12	586	77.2	144	4	AAB50871	Aab50871 Human GM-
13	586	77.2	144	4	AAB84602	Aab84602 Amino aci
14	586	77.2	144	ß	ABB05055	Abb05055 Human gra
15	586	77.2	144	Ŋ	AAU11977	Aaul1977 Human GM-
16	586	77.2	144	9	ABR55847	Abr55847 Human GM-
17	586	77.2	144	7	AAE14938	Aae14938 Human gra
18	586	77.2	144	7	ADF15243	3 Human
39	586	77.2	144	7	ADF15149	Adf15149 Human alb
20	586	77.2	144	7	ADF15242	Adf15242 Human alb
21	586	77.2	144	7	ADF15150	Adf15150 Human alb
22	586	77.2	144	7	ADH44684	Adh44684 Human GM-
23	586	77.2	144	7	ADI01020	Adi01020 Human gra

Adh10509 Human GM-	_	_	Adl16730 Human gra	Adn07713 Human G-C	Adn49690 Human gra	Adp12451 Protein e	Adp19843 Human GMC	Adq59665 Human GMC	Adr46068 Human gra	Adr46066 Human gra	Ads88047 Tumour tr	Adu74366 Human gra	Adv96467 Human GM-	-		Human	Human	Ady99886 Human imm	Adz20507 Human gra	Aeb10855 Human GM-	Aeb54698 Human col
3 ADH10509	3 ADL66118	3 ADL66120	3 ADL16730	3 ADN07713	3 ADN49690	3 ADP12451	3 ADP19843	3 ADQ59665	3 ADR46068	3 ADR46066	3 ADS88047	3 ADU74366	9 ADV96467	9 ADY19524	9 ADY16395	9 ADY84980	9 ADZ26537	9 ADY99886	9 ADZ20507	9 AEB10855	3 AEBS4698
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586	586	586	586	586	586	586	586	586	586	586	586	586	286	586	586	586	586	586	586	586	586
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

ABP98711 standard; protein; 144 AA (first entry) 27-JUN-2003 RESULT 1 ABP98711 

Equine granulocyte-macrophage colony stimulating factor.

Granulocyte-macrophage colony stimulating factor; GM-CSF; antibacterial; antivital; vaccine; animal; immunogen; DMRIE; cationic lipid; dog; cat; quaternary ammonium salt; canine distemper virus; canine herpes virus; canine parainfluenza virus; feline herpes virus;

Equus caballus.

WO200077043-A2.

21-DEC-2000.

08-JUN-2000; 2000WO-FR001592.

10-JUN-1999; 99FR-0007604. 19-JUL-1999; 99US-0144490P.

(MERI-) MERIAL.

Audonnet JF; Barzu-Le Roux S, Fischer LJ,

WPI; 2001-071259/08. N-PSDB; ABZ80828.

DNA vaccine containing plasmid and cationic lipid containing quaternary ammonium salt, useful for protecting pets and sports animals against, e.g. herpes virus.

Example 10; Fig 26; 109pp; French.

The invention relates to a novel DNA vaccine against pathogens that affect pets and sports animals comprises a plasmid containing a sequence, expressible in vivo, that encodes an immunogen from the relevant pathogen and a cationic lipid containing a quaternary ammonium salt, particularly N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium (DMRIE). The immunogens are particularly taken from canine distemper

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virus (CDV), canine parainfluenza virus type 2 (CPI-2), canine herpes virus (CHV), feline herpes virus type 1 (EHV-1), equine herpes virus type 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of a immunogenic stimulation factor especially a granulocyte-macrophage colony stimulation factor especially a granulocyte-macrophage colony stimulation factor (GM-CSF) to enhance the immunogenic response. The vaccines, which may be multivalent, are particularly used to protect dogs, cats and horses against bacterial and viral diseases, particularly those caused by the Paramyxoviridae. Formulations with the quaternary protection, particularly when administered subcutaneously. This sequence represents an equine GM-CSF used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory; granulocyte-macrophage colony stimulating factor; horse; reverse transcriptase PCR; colony formation; blood; cytotoxicity; inflammation; vector; adjuvant; immunogen; vaccination; vaccine; equine herpes; tetanus; Borrelia burgdorferi; rabies.
                                                                                                                                                                                                                                                                                                                                  1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                                                                                                                                                                                                                                                                                                       1 MWLQNLLLLCTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                                                                                                                                                                                                                                                                       Gaps
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Matches 144; Conservative
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This sequence represents a horse granulocyte-macrophage colony stimulating factor (GM-CSF). The corresponding gene was isolated from horse lymphocytes using a reverse transcriptase PCR method with primers AAPZ8954-AAFZ8950. The protein has been shown to have at least 75%

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colony formation in various types of blood cells and particularly induces colony formation in various types of blood cells and particularly induces colony formation in various types of blood cells and particularly induces and causes recruitment of leucocytes to sites of inflammation. Vectors containing the gene or the protein itself, are useful as adjuvants in immunogenic or vaccinating compositions for horses, e.g. for protection against equine herpes, tetanus, Borrelia burgdorferi, rabies etc. Also as non-specific stimulators of the immune system. In a specific example, containing the sequence for equine GM-CSF was used to transform CHO-KI cells and the transformants grown for 48 hours. The culture supernatant was then added to culture medium being used to grow containe bone marrow cells. After 14 days, the mean number of colonies per culture box was 12-15, compared with none for cells grown in absence of GM-CSF. Equine GM-CSF allows a reduction in the amount of immunogenic/vecinating component required, and may induce a response in
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                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                          Sequence 144 AA;
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27-OCT-1992
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Best Local &
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The sequence is that of a porcine cytckine designated chimerism enhancing factor (CHEF-2). The cytokine can be used for improving engrafment, stabilisation and proliferation of tissues, esp. bane marrow cells, in xenogeneic transplantation. The cytokine may be used to prevent or treat various swine diseases, e.g. African swine fever, Hog cholera, pseudorabies, etc. See also AASTS4817-9. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                    cytokine Chimerism Enhancing Factors (CHEFS) and DNA - used to
                                                                                                                              Claim 25; Page 72; 113pp; English.
                                                                            enhance xenograft tolerance.
  N-PSDB; AAQ64864.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 144 AA;
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01-JAN-1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SETFDAEELTCLQTRLKLYKQGLRGSLIKLEGPLTMMASHYKQHCPPTLETSCATQMITF 120
                                                                                                                                                 The sequence is that of the ovine granulocyte-macrophage colony stimulating factor (GM-CSF), a cytckine-like molecule. The ovine cytckines will be useful in the intensive livestock industries such as live animal export trade, feed-lots and intensive rearing industries, where animals are subjected to great environmental challenge with infectious diseases, partic. respiratory infections, and are more prone to immunodepressive effects. The cytckines may be used for treatment or prophylaxis to maintain, stimulate or enhance immunoresponsiveness. They may also be useful as natural adjuvants for vaccines for sheep and cattle. See also AAR21661-R21667. (Updated on 25-MAR-2003 to correct PA
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                        encoding ovine cytokine(s) - used to prepare recombinant cytokine(s) treatment of immuno-depression in sheep.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.5%; Score 641; DB 2; Length 144;
84.0%; Pred. No. 1.8e-61;
ive 11; Mismatches 12; Indels
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    .17
    /note= "signal peptide"

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                                                                                                     Disclosure, Fig 3; 79pp, English.
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Best Local Similarity 84.09
Matches 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 144 AA;
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10-MAR-2003
07-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocytes - useful for infectious diseases and to
                                                                            1 MWLQNLLLLGTVVCSISAPTRPPSPVTRPWQHVDAIKEALSLLNNSNDTAAVMNETVDVV
                                                                                                                                      61 CEMFDPQEPTCVQTRLNLYXQGLRGSLTRLKSPLTLLAKHYEQHCPLTEETSCETQSITF
                                                          1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The protein has GM-CSF activity and is useful in elucidating control mechanisms of mammalian immune responses. It is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                         Granulocyte, macrophage, colony stimulating factor; chemotherapy; neoplastic disease therapy; infectious disease therapy; ss.
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Length 144;
                             21; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Human granulocyte macrophage-colony stimulating factor.
77.3%; Score 587; DB 2; 76.4%; Pred. No. 1.4e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New poly:peptide(s) for colony stimulation of enhancing body defences against neoplasms and overcome myelo:suppression in chemotherapy.
                             13; Mismatches
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                                                                                                                                                                                 121 KSFKKNLKDFLFEIPFDCWKPAQK 144
                                                                                                                                                                                                  121 KSFKDSLNKFLFTIPFDCWGPVKK 144
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(first entry)
               Best Local Similarity 76.4
Matches 110; Conservative
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N-PSDB; AAN60364.
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Length 144;

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Query Match 77.29
Best Local Similarity 76.49
Matches 110; Conservative
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A recombinant DNA molecule encoding a hGM-CSF is claimed wherein there is a 5' terminal alteration allowing higher yield than the native DNA sequence. The cpds. may be used to reduce the likelihood of infections in immunologically compromised individuals, such as those suffering from AIDS by increasing their white blood cell count
                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                         Sequence of a human granulocyte-macrophage colony stimulating factor (hGM-CSF)-like polypeptide isolated from 5637 cell line.
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administration to enhance natural defences against neoplastic and infectious diseases or as an adjunct in chemotherapy to overcome myelosuppression. GM-CSF is prepared by conventional recombinant DNA techniques. The factor has activity on human neutrophilic granulocytes, macrophages and eosinophils. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                      SETFDAEELICLQTRLKLYKQGLRGSLIKLEGPLTMMASHYKQHCPPTLETSCATQMITF
                                                                                                                                          1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human granulocyte-macrophage stimulating factor-like polypeptide(s) -
produced from recombinant DNA sequence having 5' terminal alteration.
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                                                                                               77.2%; Score 586; DB 1; Length 144; 76.4%; Pred. No. 1.8e-55; Live 15; Mismatches 19; Indels
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/note= "for signal peptide"
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ESFKENLKOFLLVIPFDCWEPVQE 144
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                                                                                                                                                                                                                                                                                                                                                                                                         therapy; leukocyte; leucaemia
                                                                                                                                                                                                                                                                                                           AAP70657 standard; protein; 144
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                                                                                                Query Match
Best Local Similarity 76.4%
Matches 110; Conservative
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N-PSDB; AAN71002.
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                                                                              Sequence 144 AA;
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Sequence 144 AA;

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                                                                                                                                                                        61 SETFDABELITCLQTRLKLYKQGLRGSLIKLEGPLTMMASHYKQHCPPTLETSCATQMITF 120
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                                                                                     MWLONLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human granulocyte macrophage colony stimulating factor derivs. - for treating diseases due to leukopenia or osteomyelo-dysplastic.
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                                          19; Indels
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77.2%; Score 586; DB 1; 76.4%; Pred. No. 1.8e-55; ive 15; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSFKKNLKDFLFEIPFDCWKPAOK 144
                                                                                                                                                                                                                                                              121 KSFKKNLKDFLFEIPFDCWKPAQK 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metapyrocatechase gene product
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61 SEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITF 120

KSFKKNLKDFLFEIPFDCWKPAQK 144

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This sequence represents human granulocyte-macrophage colony stimulating factor (GM-CSF). Heterogeneity of the nucleotide sequence and the amino acid sequence has been observed and this sequence as deposited in E. coli as ATCC 19923. The GM-CSF protein was isolated using the method of the invention. The method comprises killing and disrupting GM-CSF-expressing bacteria and preparing a GM-CSF containing extract from the disrupted cells. This extract is subjected to quaternary amino ethyl (QAE) anion exchange chromatography to separate proteases and produce protease-free GM-CSF fractions. These fractions are subjected to red 120 triazinyl dyeligation affinity chromatography to obtain GM-CSF containing fractions. Free of hydrophobic impurities. These fractions are then subjected to gel filtration column chromatography to produce GM-CSF containing fractions free of high and low mol. Wt. impurities which are then subjected to gel free of high and low mol. Wt. impurities which are then subjected to gel reversed-phase column chromatography to produce fractions with a purity of greater than 95%. The obtained GM-CSF may be used in clinical situations where the stimulation of blood cell generation is desirable.
                                                                                                                                                                                                         Human; granulocyte-macrophage colony stimulating factor; GM-CSF; E.coli; quaternary amino ethyl anion exchange chromatography; red 120 triazinyl dye-ligand affinity chromatograph; gel filtration column chromatography; stimulation; blood cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purifying granulocyte-macrophage colony-stimulating factor - by eexchange, dye-ligand affinity, gel filtration and reversed-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.2%; Score 586; DB 2; Length 144; 76.4%; Pred. No. 1.8e-55; ive 15; Mismatches 19; Indels
                                                                                                                                                                       GM-CSF encoded by clone pcD-human-GM-CSF cDNA insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seelig GF, Trotta PP;
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                                    AAR71118 standard; protein; 144 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                            93US-00125356
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(first entry)
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N-PSDB; AAQ84865.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromatography
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-1993;
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                                                                                                           25-MAR-2003
12-OCT-1995
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                                                                        AAR71118;
RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                              murine
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                                                                                                                     Cytokine; mutein; granulocyte-macrophage colony stimulating factor; GM-CSF; agonist; antagonist; diagnosis; therapy; cancer; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MWLONLLLLGTVVYSMPAPTROPSPVTRPWOHVDAIKEALSLLNNSSDTAAIMNETVEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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- useful for the diagnosis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.2%; Score 586; DB 2; 76.4%; Pred. No. 1.8e-55; ive 15; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                           Mutein(s) of human and murine cytokine(s), P600 contg. amino acid substitutions. - use treatment of cancer, inflammation, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 41-42; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KSFKKNLKDFLFEIPFDCWKPAQK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR92800 standard; protein; 144 AA
                                                                                                                                                                                                                                                          95WO-US008950.
                                                                                                                                                                                                                                                                                     94US-00284393.
                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                          Zurawski
                                                                                                                                                                                                                                                                                                               (SCHE ) SCHERING CORP
                                                                                                                                                 degenerative disease
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-129335/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 144 AA;
                                                                                            Human GM-CSF
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                      WO9604306-A2
                                                                                                                                                                                                                                                            31-JUL-1995;
                                                                                                                                                                                                                                                                                    01-AUG-1994;
                                                                                                                                                                                                                                                                                                                                          Zurawski SM,
                                                                  24-MAY-1996
                                                                                                                                                                                                                               15-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders
                                       AAR92800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ID AAW
AAR92800
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AAW60031 standard; protein; 144 AA

| SETFDAEELTCLQTRLKLYKQGLRGSLIKLEGPLTMMASHYKQHCPPTLETSCATQMITF 120

MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV

Matches 110; Conservative

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61

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Gaps

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us-10-614-481-9.rag

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Amino acid sequence of a human GMCSF protein helix A fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                   This represents the human granulocyte macrophage colony stimulating factor (GM-CSF). A murine GM-CSF which is similar to the human GM-CSF is used for generating a recombinant poxvirus. The recombinant poxvirus comprises a nucleic acid sequence encoding a biological response modifier or its immunomodulating fragment in a non-essential region of the recombinant virus genome. The biological response modifier may be a cytokine, e.g. interlekin-12 (II-12), II-2 or GM-CSF. The recombinant poxvirus is used to transfect cells for expression of the biological response modifier. The products are useful for the treatment of tumours or for protecting a host against tumour formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SETFDABELICLOTRLKLYKOGLRGSLIKLEGPLTMMASHYKOHCPPTLETSCATOMITF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                             ambinant poxvirus encoding biological response modifier - useful for treatment or prevention of tumours.
                                                                                                                                                                                                                                                                 Diaz I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MWLQSLLLLGTVACSISAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                                                                        Recombinant poxvirus; biological response modifier; IL-12; GM-CSF; granulocyte macrophage colony stimulating factor; prevention; tumour; interleukin; cytokine; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                        Human granulocyte macrophage colony stimulating factor (GM-CSF).
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                                                                                                                                                                                                                                                                 Bonnet MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.2%; Score 586; DB 2; Length 144; 76.4%; Pred. No. 1.8e-55; ative 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                 Alexander J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSFKKNLKDFLFEIPFDCWKPAQK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a J, Cox B,
Klein MH;
                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 9A-F; 52pp; English.
                                                                                                                                                                                                           96US-0027530P.
                                                                                                                                                                                      97WO-CA000729
                                  (first entry)
                                                                                                                                                                                                                                 (CONN-) CONNAUGHT LAB LTD (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 110; Conservative
                                                                                                                                                                                                                                                                 DM, Tartaglia
Paoletti E, R
                                                                                                                                                                                                                                                                                                 WPI; 1998-240821/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                           N-PSDB; AAV29700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 144 AA;
                                                                                                                                                                                                                                                                  Sajewczyk DM,
                                                                                                                                                                                      03-OCT-1997;
                                                                                                                                                                                                            04-OCT-1996;
                                                                                                                      Homo sapiens
                                                                                                                                            W09815635-A2
                                  18-AUG-1998
                                                                                                                                                                  16-APR-1998.
                                                                                                                                                                                                                                                                                                                                 Recombinant
                                                                                                                                                                                                                                                                             Cornet B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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             AAW60031
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The present sequence represents part of a human GMCSF protein. It is used to produce fusion proteins with a human zalphall ligand. Zalphall ligand is useful for stimulating the proliferation and development of hematopoietic cells in vitro and in vivo. Zalphall ligand polymucleotides can be used as primers or probes to cloning the zalphall gene. The zalphall ligand is useful for treating tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for treating leukaemias and lymphomas. Antagonists against zalphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopoiesis. The zalphall ligand may also be used to stimulate an immune response against B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, polynucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis, prevention, and treatment of diseases associated with a zalphall ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SETFDABELITCLOTRIKLYKQGLRGSLIKLEGPLTWMASHYKQHCPPTLETSCATQMITF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of hematopoietic cells in vitro and in vivo, and for treating tumorigenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
zalphall ligand, cytokine; haematopoietic cell proliferation; lymphoma; tumourigenesis; leukaemia; hematopoiesis; B cell tumour; GMCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hammond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Indels
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Dillon SR, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.2%; Score 586; DB 3; 76.4%; Pred. No. 1.8e-55; ive 15; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sprecher CA,
Nelson AJ, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KSFKKNLKDFLFEIPFDCWKPAOK 144
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                                                                                                                                                                                                                                                                                                              99US-00264908.
99US-00265992.
99US-0142013P.
                                                                                                                                                                                                                                                          09-MAR-2000; 2000WO-US006067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 76.4
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Presnell (
Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-565600/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 144 AA;
                                                                                                                                                WO200053761-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic defect
                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                 09-MAR-1999;
                                                                                                                                                                                                   14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novak JE,
Gross JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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AABSO871
ID AAB:
XX
AC AAB
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AAB18633 standard; protein; 144 AA

(first entry)

22-JAN-2001

AAB18633 RESULT 11
AAB18633
ID AAB18
XX
AC AAB18
XX
DT 22-JA

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The present sequence is given in a specification relating to polynucleotide and polypeptide molecules for mammalian secreted alpha helical protein-31 (zalpha31). The polypeptides are a novel four-helixx bundle cytokine and may be used to regulate the functioning of the immune system. The polypeptides are used to identify and isolate receptors involved in spermatogenesis, steroidogenesis, testicular differentiation and regulatory control of the hypothalamic-pituitary gonadal axis, thyroid, heart and adrenal function. They are useful for treating disorders of the reproductive system, thyroid, adrenal, heart and immunological systems. Zalpha31 polypeptides, or antagonists are useful in the treatment of e.g. osteoporosis, peget's disease, and hyperparathyroidism, acute pancreatitis and gastrointestinal disorders and as analgesics, especially for bone pain. They can be used to treat atherosclerosis, pelvic inflammatory disease. (PID), psoriasis, atheritis, eczema, scleroderma and other inflammatory disease. The polypeptides, nucleic acids and/or antibodies can be used to treat heart transplantation, treat complications related to poor circulation e.g. diabetic foot ulcers, treat stroke, improve cardiac function, induce skeletal muscle neogenesis and/or hyperplasia, be used in kidney regeneration and/or for treating vistemic and pulmonary characterisminal can be used for treating viral leukaemias, hypertension. Zalpha31 can be used for treating viral leukaemias, effectively immunodeficiency syndrome (AIDS) or gastrointestinal viral
                                                                                                            granulocyte-macrophage colony stimulating factor; GM-CSF; cytostatic; antiinflammatory; antiarthritic; antirheumatoid; immunosuppressive; antiasthmatic; antibacterial; osteopathic; antibacherosclerotic; antipsoriatic; dermatological; anti-HIV; gene therapy; osteoporosis; Paget's disease; hyperparathyroidism; acute panoreatitis; gastrointestinal disorder; inflammation; heart disorder; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel 4-helix bundle cytokine, Zalpha31, useful for regulating the function of immune system and for treating thyroid, adrenal, lymphoid, inflammatory, pancreatic, blood or bone disorders.
                                                                                         Human; zalpha31; alpha helical protein-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 107-108; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000; 2000WO-US014795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0136485P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-070967/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                       40200073458-A1
                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-1999;
                                             Human GM-CSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conklin DC;
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                                                                               1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV 60
                                                                                                                       1 MWLQSLLLLGTVACSISAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVI
                                         Gaps
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77.2%; Score 586; DB 4; Length 144; 76.4%; Pred. No. 1.8e-55;
                                       19; Indels
                                       15; Mismatches
                                         Matches 110; Conservative
                       Similarity
                         Best Local
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1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV 60

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The specification describes a pharmaceutical composition, comprising a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent inhibitor agent inhibitor agent action of at least one specific adverse protein, i.e. a protease, that is upregulated in a damaged tissue such as a wound invention are platelet rederived growth factor (PGF), it is blatelet derived growth factor (FGF), connective tissue derived growth factor (CTGF), keratinocyte-derived growth factor (KGF), transforming growth factor-beta (TGF-bera), granulocyte macrophage colony stimulating factor (GM-CSF), epidermal growth factor (GGF), and chrysalin. Inhibitors which are included in the composition of the invention included inhibitors of urokinase-type plasminogen activator (UPA) and matrix metalloproteinase (MMP). The composition is useful for the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
                                                                                                                                                                                                                                                     Growth factor; protein inhibitor; protease; damaged tissue; platelet-derived growth factor; PDGF; fibroblast growth factor; FGF; connective tissue derived growth factor; CTGF; chrysalin; VEGF; keratimocyte-derived growth factor; KGF; epidermal growth factor; EGF; transforming growth factor-beta; TGF-bata; matrix metalloproteinase; MMP; granulcoyte macrophage colony stimulating factor; GM-CSF; uPA; dermal ulcer; wound.
                                                                                                                                                                                                                             Amino acid sequence of granulocyte macrophage colony stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition for the treatment of damaged tissue i.e. chronic wounds and dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Occleston NL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.2%; Score 586; DB 4; 76.4%; Pred. No. 1.8e-55; iive 15; Mismatches 19
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                121 KSFKKNLKDFLFEIPFDCWKPAQK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 548; 572pp; English.
                                                                                                                       AAB84602 standard; protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the composition of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-2000; 2000WO-IB001935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-00030768.
                                                                                                                                                                                            (first entry)
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Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davies MJ, Huggins JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-418351/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH28217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200149309-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-1999;
                                                                                                                                                                                              05-SEP-2001
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                                                                                                                                                          AAB84602;
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121 KSFKKNLKDFLFEIPFDCWKPAQK 144
                       AAU11977 standard; protein; 144 AA
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Gross JA,
                                                                                                                 AAU11977;
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                                                                     RESULT 15
                                                                                 AAU11977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for producing human granulocyte macrophage colony stimulating factor (hGM-CSF), where hGM-CSF having higher activity is easily purified. The method comprises: (a) preparing a fusion gene construct which contains a human origin glycoprotein gene linked with a bladder specific promoter, uroplakin II; (b) microinjecting the fusion gene construct into a fertilised egg; (c) transplanting the egg containing the fusion gene construct (KCTC 0723BP) into a surrogate mother; (d) producing a transformed animal KCTC 0723BP) into a surrogate mother; (d) producing a transformed animal from the surrogate mother; and present inequence represents hGM-CSF which his referred to using the Genbank accession number X03021 in the exemplification of the present invention. N.B. The present is not given in the specification
                                   61 SEMPDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTWMASHYKQHCPPTPETSCATQIITF 120
                       SETFDAEELTCLQTRLKLYKQGLRGSLIKLEGPLTMMASHYKQHCPPTLETSCATQMITF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
1 MWLQSLLLLGTVACSISAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing human granulocyte/macrophage colony-stimulating factor comprises purifying the factor from the urine of a transformed animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                              Human, granulocyte macrophage colony stimulating factor; GM-CSF; fusion gene; glycoprotein; bladder specific promoter; uroplakin II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                        Human granulocyte macrophage colony stimulating factor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ryu JU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.2%; Score 586; DB 5; Length 144; 76.4%; Pred. No. 1.8e-55; ive 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee JU, Park YI,
                                                                                   121 KSFKKNLKDFLFEIPFDCWKPAQK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim TY,
                                                                                                                                                    ABB05055 standard; protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   BIO CLUE & SOLUTION CO LTD. KIM T Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page; 20pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000; 2000KR-00005437.
                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000; 2000KR-00005437.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim MO,
                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABA92719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 144 AA;
                                                                                                                                                                                                                                                                                                        KR2001077563-A.
                                                                                                                                                                                                                                                                                  Homo sapiens
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calphall Ligand and the polymucleotide encoding it. The invention also gives the sequence for the zalphall receptor and the polymucleotide encoding it. The zalphall Ligand polypetide stimulates proliferation of natural killer (NK) cells or NK cell progenitors, the activation of NK cells, proliferation of T-cells, proliferation of B-cells stimulated with anti-control of natural killer (NK) cells or NK cells progenitors, the activation of NK cells, proliferation of B-cells stimulated with anti-control of not or stimulated with anti-control of not or calphall Ligand polypetide is also useful in preparing antibodies. The calphall Ligand polymucleotides can be used as probes or primers to clone regions of a zalphall Ligand gene, and in gene therapy. Zalphall Ligand may also be used to identify inhibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to activate or stimulate the immune system. The present sequence representing human GM-CSF (granulocyte macrophage-colony stimulating factor) polypetide can be used to create fusion proteins containing the next of the next of create fusion proteins containing the next of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New zalphall ligand polypeptides and polynucleotides, useful for
stimulating proliferation, activation, differentiation and/or induction
of inhibition of specialized cell function, or for stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                           Cytokine, zalphall Ligand, zalphall receptor, NK cell progenitor; natural Killer cell proliferation; human; human; B-cell proliferation; anti-tumour response; immune system; GM-CSF; immunostimulant; granulocyte macrophage-colony stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DC, Holly Hammond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.2%; Score 586; DB 5; Length 14 76.4%; Pred. No. 1.8e-55; ive 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA, Foster DC
J, Dillon SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 191-192; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sprecher CA
Nelson AJ,
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99US-0123904P.
99US-0142013P.
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                                                                                                  Human GM-CSF polypeptide.
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Johnston JV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-040208/05.
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01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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09-APR-2002
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120

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61 SEMFDLOEPTCLOTRLELYKOGLRGSLTKLKGPLTMMASHYKOHCPPTPETSCATOIITF 120

61 SETFDAEELTCLOTRLKLYKQGLRGSLIKLEGPLTMMASHYKQHCPPTLETSCATQMITF

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6 B 6 B 6
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<sup>121</sup> KSFKKNLKDFLFEIPFDCWKPAQK 144 :|||:||||||||||||||11 121 ESFKENLKDFLLVIPFDCWEPVQE 144

Search completed: May 25, 2006, 14:55:49 Job time : 199 secs

DEST AVAILABLE COPY

GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.

- protein search, using sw model OM protein May 25, 2006, 14:56:07; Search time 39 Seconds Run on:

(without alignments)
355.262 Million cell updates/sec

US-10-614-481-9

Perfect score:

1 MWLQNLLLLCTVVYSMPAPT......KNLKDFLFEIPFDCWKPAQK 144 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR 80:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S Description		granulocyte-macrop	hypothetical coile	acetylornithine am	DNA-directed DNA p	acyl-CoA desaturas	acyl-CoA dehydroge	FUN21 protein - ye	probable receptor-	probable tRNA-guan	phage infection pr	DNA-directed DNA p	probable mitochond	hexose transport p	gene MSSP-2 protei	SREBP cleavage act		hypothetical prote	hypothetical prote	phage infection pr		hypothetical prote	sensory transducti	DNA-directed DNA D						
SUMMARIES ID		A61632	CHU469	FOHUGM	FQBOGM	A44936	FOMSGM	146269	T39964	F69476	B42543	F97707	G90465	S70294	E84429	A96556	F86833	T17675	G86383	S46724	S53612	T18526	T03022	B83695	G83901	A48653	836512	T20706	S75662	A42543
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% Query Match	1 1 1	4. 4.	83.7	77.2	75.7	74.6	59.4	59.0	11.1	10.7		٠		10.3	10.3	10.1	10.1	10.1	10.0	10.0	6.6	9.6		9.7	9.7	9.6	9.6	•	9.6	9.6
Score		641	63/	586	574.5	995	450.5	448	84.5	81.5	79.5	78.5	78.5	78.5	78.5	77	77	76.5	16	97	75	74.5	74	73.5	73.5	73	72.5	72.5	72.5	72.5
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F84559	H81979	B96492	T30334	T10236	T30273	JS0512	G87536	F64334	A42220	S54525	D81522	C86608	G72017	D82246	A59233
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167	187	884	1127	1364	1450	208	312	591	644	169	828	828	828	1088	2121
9.5	9.5	9.5	9.5	9.5	9.5	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4
72	72	72	72	72	72	71	71	71	71	71	71	71	71	71	71
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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RESULT 1
A61632
granulocyte-macrophage colony-stimulating factor precursor - sheep
Granulocyte-macrophage colony-stimulating factor precursor - sheep
Granulocyte-macrophage colony-stimulating factor precursor - sheep
C;Species: 0.0-sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004
C;Accession: A61632
Immunol. Cell Biol. 69, 51-55, 1991
A;Ttle: Cloning and sequencing of the cDNA for owine granulocyte-macrophage colony-stimulatie: Cloning and sequencing of the cDNA for owine granulocyte-macrophage colony-stimulation. A61632
A;Accession: A61632
A;Cossorice Compared with conceptual translation
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ö Gaps ö Length 144; 12; Indels 84.5%; Score 641; DB 1; 84.0%; Pred. No. 3.9e-54; iive 11; Mismatches 12; Query Match Best Local Similarity 84.0° Matches 121; Conservative

60 1 MWLQNLLLLGTVVCSFSAPTRQPSPVTRPWQHVDAIKEALSLLNDSTDTAAVMDETVEVV 60 1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV ò 셤

g

121 KSFKKNLKDFLFEIPFDCWKPAQK 144 121 ò g

# RESULT 2 JH0469

granulocyte-macrophage colony-stimulating factor precursor - sheep
N;Alternate names: colony-stimulating factor 2; GM-CSF
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004
C;Accession: JH0469; S16730
R;McInnes, C.J; Haig, D.M.
GRH 105, 275-279, 1991
A;Title: Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-st
A;Title: Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-st
A;Title: Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-st
A;Title: Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-st
A;Toss-references uniper: JH0469
A;Accession: JH0469
A;Accession: JH0469
A;Residues: 1-144 <MCI>A;Cross-references uniper: JH050000128522; GB:X53561; NID:g1800; PIDN<sub>3</sub>CA
C;Comment: This protein is a glycoprotein cycokine produced and secreted by various cell
C;Superfamily: granulocyte-macrophage colony-stimulating factor

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A; Residues: 1-116, T', 118-144 < WON>
A; Residues: 1-116, T' (118-144 < WON>
A; Cross-references: UNIPARC: UP10000142467; GB: M10663; NID: 9181145; PIDN: AAA52121.1; PID:
A; Note: parts of this sequence, including the amino end of the mature protein, were conf
R; Wen, D.Y.; Huang, B.R.; Cai, L.W.; Si, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         granulocyte-macrophage colony-stimulating factor precursor [validated] - human N;Alternate names: colony-stimulating factor 2; GM-CSF (Species: Homo sapiens (man) (Species: O4-Dec-1986 #sequence revision 04-Dec-1986 #text change 09-Jul-2004 (Spacession: C24636; I59065; A25169; A01853; A44175; JC1090 (Species: No. Otsuka, T.; Yokota, T.; Lee, F.; Arai, K. EMBO J. 4, 2561-2568, 1985 (Arai, R.) (Arai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-144 <AIIV.
A; Residues: 1-144 <AIIV.
A; Residues: 1-144 <AIIV.
A; Residues: 1-144 <AIIV.
A; Cross-references: UNIPROT: P04141; UNIPARC: UPI00000358DB; EMBL: X03021; NID: 931858; PIDN
B; Kaushansky, K.; O'Hara, P.J.; Berkner, K.; Segal, G.M.; Hagen, F.S.; Adamson, J.W.
R; Kaushansky, K.; O'Hara, P.J.; Berkner, K.; Segal, G.M.; Hagen, F.S.; Adamson, J.W.
A; Title: Genomic Sci. US.A. 83, 3101-3105, 1986
A; Title: Genomic cloning, characterization, and multilineage growth-promoting activity c
A; Reference number: IS9065; MUID: 86205844; PMID: 3486413
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: UNIPARC:UPI00000158DB; GB:M13207; NID:g181147; FIDN:AAA98768.1; PID:
B;Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R.
B;Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R.
A;Contrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R.
A;Title: Cloning, sequence, and expression of a human granulocyte/macrophage colony-stim
A;Reference number: A25169; MUID:85298329; PMID:3898082
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A; Title: Isolation of cDNA for a human granulocyte-macrophage colony-stimulating factor A; Reference number: A01853; MUID:85242684; PMID:3925454
A; Recession: A01853
A; MuID:85242684; PMID:3925454
A; Molecule type: mRNA
A; Residues: 1-144 < LEE>
A; Cross-references: UNIPARC:UPI00000358DB; GB:M11220; NID:G183363; PIDN:AAA52578.1; PID: R; Wong, G.G.; Witek, J.S.; Temple, P.A.; Wilkens, K.M.; Leary, A.C.; Luxenberg, D.P.; JG
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Science 228, 810-815, 1985
A;Title: Human CM-CSF: molecular cloning of the complementary DNA and purification of th
A;Reference number: A44175; MUID:85218749; PMID:3923623
                                                                                                           √M.≻
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell F;1-17/Domain: signal sequence #status predicted <SIG> F;18-144/Product: granulocyte-macrophage colony-stimulating factor #status predicted F;44/Binding uite: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                           Length 144;
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                                                                                                                                                                                                                                                                      Score 637; DB 2;
Pred. No. 9.4e-54;
                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
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KSFKENLKDFLFIIPFDCWEPVQK 144
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                                                                                                                                                                                                                                                                      83.9%;
83.3%;
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A; Residues: 1-144 <CAN>
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Best Local
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Fuzzoura proposed colony-stimulating factor precursor - bovine
NyAlternate names: colony-stimulating factor 2; GM-CSF
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar.1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
Mol: Immunol. 25, 843-850, 1988
Mol: Immunol. 25, 845-850, 1988
Mol: Immunol. 26, 845-850, 1988
M
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                                                                       wit
Acta Biochim. Biophys. Sin. 25, 651-655, 1993
A;Title: Amplification of human granulocyte-macrophage colony-stimulating factor cDNA varitle: Amplification of human granulocyte-macrophage colony-stimulating factor cDNA vareession: JC1090
A;Reference number: JC1090
A;Molecule type: protein
A;Residues: 18-21, C', 23-96, 'L', 98-144 <WEN>
A;Cross-references: UNIPARC:UP1000017368E
C;Genetics:
A;Gene: GDB:119812; OMIM:138960
A;Map position: 5q23.2-5q31.1
A;Introns: 53/3; 67/3; 109/3
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75.7%; Pred. No. 8.9e-48;
iive 16; Mismatches 18
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Matches 110; Conservative
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nes 109; Conservative
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A, Molecule type: DNA
A, Assables: 13150, G'1,12-153 «STA>
A, Molecule type: DNA
A, Residues: 13150, G'1,12-153 «STA>
A, Residues: 13150, G'1,12-153 «STA>
A, Residues: 13150, G'1,12-153 «STA>
A, Cross-references: UNIPARC.UPFO00002164F; GB:X03020; NID:g51098; PIDN:CAA26821.1; PID:g5
B, Delamarter, U. F.; Mermad, U.J.; Liang, C.M.; Eliason, J.F.; Thatcher, D.R.
B, Med O, 4, 2575-2581 1995
A, Residues: 134644; MUID:86030236; PMID:3902470
A, Accession: AA4644
A, Molecule type: MRNA
A, Residues: 13153 «BDA
A, Recenter unuber: A24644; MUID:84030236; PMID:3902470
A, Riccoss-references: UNIPARC.UP1000016615F; GB:X03019; NID:g51100; PIDN:CAA26820.1; PID:g5
B, Googh, N.M.; Googh, U. M.; Metcalf, D.; Kelso, A.; Grail, D.; Nicola, N.A.; Burgess, A.W.;
A, Molecule type: MRNA
A, Residues: 36, 11, 38-150, 15, 152-153 «GOU»
A, Accession: A01854
A, Molecule type: MRNA
A, Residues: 36, 11, 38-150, 15, 152-153 «GOU»
A, Cross-references: UNIPARC.UP10000157579; GB:X05906; NID:g51096; PIDN:CAA29336.1; PID:g5
A, Cross-references: UNIPARC.UP10000157579; GB:X05906; NID:g51096; PIDN:CAA29336.1; PID:g5
A, Title: Purification and partial amino acid sequence of asialo murine granulocyte-macrop
A, Roccession: A1882; MUID:8513187; PMID:3871523
A, Title: Purification and partial amino acid sequence of asialo murine granulocyte-macrop
A, Accession: A1882; MUID:8513187; PMID:3871523
A, Molecule type: protein
A, Residues: 36, 17, 38-69 «SPA
A, Cross-references: UNIPARC.UP1000017368F
A, Cross-references: UNIPARC.UP100001776F
C, Genetics:
C, Genetic
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Residues: 1-127 <SNIA
A;Residues: 1-127 <SNIA
A;Residues: UNIPROT:P48750; UNIPARC:UPI000004361B; EMBL:U00620; NID:g392779; PIDNC;Superfamily: granulocyte-macrophage colony-stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         granulocyte-macrophage colony stimulating factor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146269
R;Smith, D.R.; Lundeen, K.A.; Diveley, J.P.; Carlo, D.J.; Brostoff, S.W.
A;Title: Nucleotide sequence of the Lewis rat granulocyte-macrophage colony stimulating
A;Reference number: 146269; MUID:94041474; PMID:8225444
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Pred. No. 1e-35;
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64.6%;
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les 86; Conservative
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                                                                                                                                                                          granulocyte-macrophage colony-stimulating factor precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A44936
R;Nash, R.A.; Schuening, F.; Appelbaum, F.; Hammond, W.P.; Boone, T.; Morris, C.F.; Slic
Blood 78, 930-937, 1991
A;Title: Molecular cloning and in vivo evaluation of canine granulocyte-macrophage colon
A;Reference number: A44936
A;Accession: A44936
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA; mRNA
A;Residues: 13-150, 'G',152-153 <MIY>
A;Cross-references: UNIPARC:UPI00002164F; GB:X03020; NID:g51098; PIDN:CAA26821.1; PID:g
A;Orce: the sequence translated from the mRNA differs from that of the DNA in having 151
R;Stanley, E.; Metcalf, D.; Sobieszczuk, P.; Gough, N.M.; Dunn, A.R.
EMBO J. 4, 2569-2573, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID
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Babo J. 4, 2561-2568, 1985
A;Title: Structure of the chromosomal gene for granulocyte-macrophage colony stimulating
A;Reference number: A91015; MUID:86030234; PMID:3876930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The structure and expression of the murine gene encoding granulocyte-macrophage A;Reference number: A24645; WUID:86030235; PMID:3876931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P01587; UNIPARC:UPI000016CD8F; EMBL:X02333; NID:951103; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P48749; UNIPARC:UP1000012851D; GB:S49738; NID:g233566; PIDN:
A;Note: sequence extracted from NCBI Dackbone (NCBIN:49738, NCBIP:49739)
C;Superfamily: granulocyte-macrophage colony-stimulating factor
F;1-17/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        granulocyte-macrophage colony-stimulating factor precursor - mouse
N;Alternate names: colony-stimulating factor 2; GM-CSF; integral membrane protein
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: 148368; 148368; A24636; A24644; A01854; A21882
R;Gough, N.M.; Metcalf, D.; Gough, J.; Grail, D.; Dunn, A.R.
A;Title: Structure and expression of the mRNA for murine granulocyte-macrophage colony
A;Reference number: 148368; MUID:85230531; PMID:3874057
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Residues: 13-153 <RE2>
Cross-references: UNIPARC:UPI000016615F; EMBL:X02333; NID:951103; PIDN:CAA26193.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.6%; Score 566; DB 2; 73.6%; Pred. No. 5.9e-47; ive 16; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-153 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: I48369
Status: preliminary; translated from GB/EMBL/DDBJ
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KNFKEDLKEFLFIIPFDCWEPAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 73.6
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-144 <NAS>
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Matches

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A,Cross-references: UNIPROT:Q92JK5; UNIPARC:UPI00000CBC8D; GB:AE006914; PIDN:AAL02600.1;
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acyl-CoA desaturase 1 [imported] - Rickettsia conorii
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004
C;Accession: F97707
Science 293, 2093-2099, 2001
A;Ritle: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Reference preliminary
A;Molecule type: DNA
A;Residues: 1-397 <KUR>
A;Residues: 1-307 <KUR>
                                                                                                            209 PEDFYRRVREICD--EKGCLMIMDEVQTGL-----GRTGKMWGIE------HYKV-VP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 -----VSETFDABELICL----QTRLKLYKQGLRGSLIKLEGPLTMMASHYKQHCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ROPSPVTRPWOHVDAIKEALSLLNNSSDTAAIMNETVEVVSETFDAEELTCLOTRLKLYK
                                                                                  7 LLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEV-----
                                             Gaps
                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
Query Match 10.7%; Score 81.5; DB 2; Length 424; Best Local Similarity 27.3%; Pred. No. 5.1; Matches 42; Conservative 15; Mismatches 52; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                       107 PTLET----SCATQMITFKSFKKNLKDFLFEIPF 136
                                                                                                                                                                                                                                                                                            253 DVIVTAKGLSGGVYPİSATCFKEGLDDFMAENPF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 QGLRGSLIKLEGPLTMMASHYKQHCPPTLETS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   777 TG-----------YKNECQPHLHVS 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 79.5;
ilarity 28.3%; Pred. No. 19
Conservative 8; Mismatche
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C;Superfamily: acyl-CoA desaturase
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Best Local Similarity
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Best Local S
Matches 26
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C;Superfamily: beta-alanine-pyruvate transaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: UNIPROT:060187; UNIPARC:UPI0000135984; EMBL:AL023779; PIDN:CAA19316; Experimental source: strain 972h-; cosmid c244
                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T39964
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Wambutt, R.; Wedler, submitted to the EMBL Data Library, June 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
      ö
                                                                                                                                                     61 LYKQGLRGNLTKLNGALTMIASHYQTNCPPTPETDCEIEVTTFEDFIKNLKGFLFDIPFD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 LONRNVHLETVPESYPVPPSGYPLTSSTCVSSISQPIQSTDCQKAQENLSNNKQMSSNDQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----0I 348
                                                                                                                              78 LYKQGLRGSLIKLEGPLIMMASHYKQHCPPTLETSCATQMITFKSFKKNLKDFLFEIPFD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LONL-LLLGTVVYSMPAP-----TRQPSPVTRPWQHVDAIKEALSLLNN---SSDTA 50
                                             77
                                                                         51 AI--------MNETVEVVSETFDAEELTCLQTRLKLYKQGLRGSLIKL 90
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                                                                                                                                                                                                                                                                                                                                                                nypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                               18 APTROPSPVTRPWOHVDAIKEALSLLNNSSDTAAIMNETVEVVSETFDAEELTCLQTRLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.1%; Score 84.5; DB 2; 24.2%; Pred. No. 4.4; ive 22; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Conservative
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: Z21894
A;Accession: T39964
                                                                                                                                                                                                                  CWKPAOK 144
                                                                                                                                                                                                                                                       CWKPVQK 127
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1-660 < LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 2
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91

Matches

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Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT:Q9SIT1; UNIPARC:UP100000A814B; GB:AE002093; NID:g4522003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653 IKRVRF----AGV-PPMTEAENPKPTKVGWYKKPAVLHYPP-IPASAMIKPLQHKSKYNT 706
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A;Note: this sequence has been revised in reference S70291
A;Note: this sequence has been revised in reference S70291
A;Note: this sequence bNA
A;Residues: 1-96,'KVP',104,'A',106,'SIPADKAK',115,'SAAEI',121,'N' <BUF>
A;Cross-references: UNIPARC:UP100001792FA; EMBL:U12980
A;Note: this sequence has been revised in reference S70291
C;Genetics:
A;Gene: SGD:FUN21
A;Cross-references: SGD:S0000029; MIPS:YAL031C
A;Map position: 1L
C;Superfamily: Saccharomyces cerevisiae FUN21 protein
C;Keywords: transmembrane #status predicted <TM1>
F;194-210,Domain: transmembrane #status predicted <TM2>
F;287-303/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 SMPAPTRQ----PSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVVSETFDAEELT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 10.3%; Score 78.5; DB 2; Length 760; Best Local Similarity 27.0%; Pred. No. 20; Matches 37; Conservative 23; Mismatches 48; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 943;
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10.3%; Score 78.5; D
Best Local Similarity 35.6%; Pred. No. 25;
Matches 21; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 ----- FKKNLKDFL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 127-760 <BUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-943 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: At2g01820
A·Man position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           acyl-CoA dehydrogenase (acd-6) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 2-4-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accssion: G90465
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-760 <NOD>
A; Cross-reterences: UNIPROT: P39732; UNIPARC: UPI000013A02E; EMBL: U12980; NID: 91326053; PI
A; Cross-reterences: UNIPROT: P39732; UNIPARC: UPI000013A02E; EMBL: U12980; NI; Hall, J.; Ouel
R; Busesy, H.; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; Ouel
submitted to the EMBL Data Library, August 1994
A; Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.
A; Reference number: $51956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-400 «KUR»
A;Cross_references: UNIPROT:Q97UW6; UNIPARC:UPI00000648A2; GB:AE006641; NID:g13816236;
  <u>ب</u>
                                                                                                    226 IWWMALFLIGENWHNYHHAFPSDYRNGA----KWYHLDVHKWIIFLMSKIGLASELERTT 281
                                                                                                                                                                                            282 KVRIQAKMQETLNYLSEK-QKQKLTLMQTKIDHLLENLCLKIKELEESSITIKEQFKKSF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
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                                                      48
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                                                                                                                                                             49 ---TAAIMNETVEVVSETFDAEELICLOTR-----LKL----YKQGLRGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 YVVTARTSPPEPNARWKGISMFIVEREWKGVKVLNRIETMGLRASNTAELAFEDVEVPAE
                                                      MWLQNLLLLG----TVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNN---SSD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 YSMPAPTRQPSP-----VTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVVSE
  Gaps
  49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 400;
45; Indels
                                                                                                                                                                                                                                                                         IKLEGPLTMMASHYKQHCPPTLETSCATQMITFKSFKKNLK 128
                                                                                                                                                                                                                                                                                                            10.3%; Score 78.5; DE
22.9%; Pred. No. 9.2;
:ive 23; Mismatches
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNZI protein - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YAL031c C;Species: Saccharomyces cerevisiae C;Date: 06-Sep-1996 #sequence revision 06-Sep-19 C;Accession: S70294; S51989; S53563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Vo, D
submitted to the EMBL Data Library, April 1996
KReference number: S70291
A;Accession: S70294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 TOMITEKSFKKNLKDFLFEI 134
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287 --LIGFQMVQEKIAESLTEV 304
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40; Conservative
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Best Local Similarity
Matches 32; Conserv
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A;Status: preliminary
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Huntor, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rizzo, M.; Roonsy, T.; Rowley, D.; Sakano, H.
A;Authors: Salzaberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719; PMID:11130712
A;Accession: A96556
A;Status: preliminary
A;Residues: 1-490
A;Residues: 1-490
A;Cross-references: UNIPROT:Q9C8H9; UNIPARC:UPI00000A4D88; GB:AE005173; NID:g11094755; FC;Genetics:
A;Genetics:
A;Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 ISKCTLHCQESGEESSETESVYSLKCHISHEVNHLHEGL---KHGLKGELEKTSPALGRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ALSLLNNSSDTAA 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.1%; Score 77; DB 2; Length 490;
Best Local Similarity 26.6%; Pred. No. 16;
Matches 38; Conservative 14; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 WLONLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : |: | : |
ALYVKESLIDSLPRYLTVQFVRF 319
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RESULT 1
US-09-587-964-8
; Sequence 8, Application US/09587964
; GENERAL INFORMATION:
Score
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                                                                                                                                       May 25, 2006, 15:01:52 ; Search time 599 Seconds (without alignments) 367.081 Million cell updates/sec
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1: FBMC_Celerra_SIDS3/ptodata/2/paa/US066_COMB.pep:*

2: FBMC_Celerra_SIDS3/ptodata/2/paa/US076_COMB.pep:*

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8: FBMC_Celerra_SIDS3/ptodata/2/paa/US076_COMB.pep:*

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14: FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

15: FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

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16: FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

17: FBMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*

18: FBMC_Celerra_SIDS3/ptodata/2/paa/US096_COMB.pep:*

18: FBMC_Celerra_SIDS3/ptodata/2/paa/US096_COM
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759
1 MMLQNLLLLGTVVYSMPAPT.......KNLKDFLFEIPFDCWKPAQK 144
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pep: *
                   GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect
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Sequence 8, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 55369, A
Sequence 55369, A
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Sequence 82598, A
Sequence 101680,
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Sequence 24, Appl
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Sequence 15, Ap
Sequence 39311,
Sequence 18, Ap
                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17,
Sequence 15,
Sequence 553
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              /EMC_Celerra_S1DS3/ptodata/2/paa/US600_COMB.pep:*
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/EMC_Celerra_S1DS3/ptodata/2/paa/US604_COMB.pep:*
/EMC_Celerra_S1DS3/ptodata/2/paa/US606_COMB.pep:*
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COMB.
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S US-10-614-4811-9

S US-11-301-800-10

VS-09-791-537-98077

VS-09-791-537-98027

VS-09-791-537-69622

VS-09-791-537-69622

VS-09-791-537-69622

VS-09-791-537-69622

VS-09-791-537-69622

VS-09-791-537-69680

VS-11-301-800-12

PCT-US00-06067-114
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US-08-284-393-11
US-08-284-393-11
US-09-580-474A-17
US-09-726-295-15
US-10-116-275-217
US-10-116-275-217
US-10-170-205E-39311
US-10-217-994-18
US-10-311-755-27
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US-10-410-897-18
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PCT-USOZ-40891-540
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PCT-USOZ-11246-2460
PCT-USOZ-11346-2460
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PCT-USOZ-31827-83
PCT-USOZ-11494-18
PCT-USOZ-11494-18
PCT-USOZ-11494-18
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Match Length
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# ALIGNMENTS

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LENGTH: 144
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GENERAL INFORMATION:

APPLICANT: Fischer, et al.

TILE OF INVENTION: IMPROVED DNA VACCINES FOR PETS

FILE REFERENCE: 454313-2530.1

CURRENT APPLICATION NUMBER: US/09/587,964A

CURRENT FILING DATE: 2000-06-06

PRIOR FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 83

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8
APPLICANT: Fischer, et al.

TITLE OF INVENTION: IMPROVED DNA VACCINES FOR PETS FILE REFERENCE: 454313-2530.1

CURRENT APPLICATION NUMBER: US/09/587,964

CURRENT FILING DATE: 2000-06-06

PRIOR APPLICATION NUMBER: US 60/144,490

PRIOR APPLICATION NUMBER: 1999-07-19

NUMBER OF SEQ ID NOS: 79

SOFTWARE: Patentin version 3.0
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Best Local Similarity 100.0
Matches 144; Conservative
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ORGANISM: Equus sp.
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US-09-587-964A-8
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US-11-301-800-10
is 201-800-10
is Sequence 10. Application US/11301800
is GENERAL INFORMATION:
APPLICANT: BUELOW, ROLAND
TITLE OF INVENTION: IMPROVED DNA IMMUNIZATION WITH
TITLE OF INVENTION: RECOMBINASE/TRANSPOSASE
FILE REPERENCE: 39691-0013
CURRENT APPLICATION NUMBER: US/11/301,800
CURRENT FILING DATE: 2005-12-12
PRIOR APPLICATION NUMBER: US 60/636,361
PRIOR PILING DATE: 2004-12-14
NUMBER: OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 146
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TITLE OF INVENTION: Equine GM-CSF
FILE REFERENCE: 454313-2334.1
CURRENT APPLICATION NUMBER: US/10/614,481
CURRENT FILING DATE: 2003-07-07
PRIOR APPLICATION NUMBER: US/09/589,460
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 9
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                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Equine sp.
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ORGANISM: Equus
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RESULT 5 US-09-791-537-98077

Sequence 9, Application US/10614481; GENERAL INFORMATION:
APPLICANT: Bublot, et al.

RESULT 3 US-10-614-481-9

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Sequence 69622, Application US/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Denser, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 153055
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BUELOW, ROLAND
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION WITH
TILE OF INVENTION: RECOMBINASE/TRANSFOGASE
FILE REFERENCE: 39691-0013
CURRENT APPLICATION NUMBER: US/11/301,800
CURRENT FILING DATE: 2005-12-12
PRIOR FILING DATE: 2005-12-14
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PASTERCE FOR Windows Version 4.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 633; DB 27; 1
Pred. No. 8.9e-63;
7; Mismatches 16;
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84.0%; Pred. No. 8.9e-63;
tive 7; Mismatches 16;
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84.0%;
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Best Local Similarity 84.0
Matches 121, Conservative
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Matches 121; Conservative
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; ORGANISM: Cervus elaphus
US-09-791-537-69622
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ORGANISM: Cervus
            US-09-791-537-69622
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Sequence 98077, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARES: PatentIn version 3.0
SEQ ID NO 98077
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GENERAL INFORMATION:
APPLICANT: Bonomix, Inc.
APPLICANT: Debe, Derek
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83.9%; Score 637; DB 27; Length 14
Best Local Similarity 83.3%; Pred. No. 3.1e-63;
Matches 120; Conservative 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
84.5%; Score 641; DB 27;
Best Local Similarity 84.0%; Pred. No. 1.1e-63;
Matches 121; Conservative 11; Mismatches 12;
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CORGANISM: Ovis aries
US-09-791-537-98077
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SETFDAEELTCLOTRLKLYKQGLRGSLIKLEGPLTWMASHYKQHCPPTLETSCATOMITF 120
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TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND
FILE REFERENCE: 99-16PC
CURRENT APPLICATION NUMBER: PCT/USO0/0667
CURRENT APPLICATION NUMBER: DS 09/264,908
EARLIER REPLICATION NUMBER: US 09/264,908
EARLIER PELLICATION NUMBER: US 09/265,992
EARLIER PELLICATION NUMBER: US 09/265,992
EARLIER PILLING DATE: 1999-03-01
SEARLIER PELLING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                           APPLICANT: PLATZER, JOSEF
TITLE OF INVENTION: IMPROVED DNA IMMUNIZATION WITH
TITLE OF INVENTION: RECOMBINASE/TRANSPOSASE
FILE REPERBNCE: 39691-0013
CURRENT APPLICATION NUMBER: US/11/301,800
CURRENT FILING DATE: 2005-12-12
PRIOR APPLICATION NUMBER: US 60/636,361
PRIOR PILING DATE: 2004-12-14
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 144
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                                                                      ; Sequence 12, Application US/11301800
; GENERAL INFORMATION:
; APPLICANT: BUELOW, ROLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 76.4 Matches 110; Conservative
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PCT-US00-06067-114
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ORGANISM: Sus
   RESULT 11
US-11-301-800-12
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LENGTH: 144
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PAPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                       Sequence 82598, Application US/09791537
GREERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bebe, Derek
APPLICANT: Debc, Derek
APPLICANT: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: HETHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PALENCH VERSION 3.0
SEQ ID NO 82598
LENGTH: 144
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; Pred. No. 1.5e-57;
13; Mismatches 21; Indels (
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Best Local Similarity 76.4%
Matches 110; Conservative
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US-09-791-537-101680
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US-09-791-537-82598
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-09-791-537-82598
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                  Length 144;
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76.4%; Pred. No. 1.9e-57;
iive 15; Mismatches 19
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564PCT
CURRENT APPLICATION NUMBER: PCT/US02/40891
CURRENT FILING DATE: 2002-12-23
               PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 144
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ESFKENLKDFLLVIPFDCWEPVOE 144
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PRIOR APPLICATION NUMBER: 60/341,811
PRIOR PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/346,000
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-8
PRIOR FILING DATE: 2002-03-9
PRIOR FILING DATE: 2002-03-9
PRIOR PILING DATE: 2002-01-4
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-11
PRIOR PILING DATE: 2002-10-12
PRIOR PILING DATE: 2002-10-23
PRIOR PILING DATE: 2002-10-23
PRIOR PILING DATE: 2002-10-23
PRIOR PILING DATE: 2002-10-23
PRIOR PILING DATE: 2002-11-05
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PRIOR PILING DATE: 2002-11-05
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   2002-10-28
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Best Local Similarity 76.4°
Matches 110; Conservative
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Best Local Similarity 76.4
Matches 110; Conservative
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ORGANISM: Homo sapiens
PCT-US02-34502-10
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ORGANISM: Homo sapiens
CURRENT FILING DATE:
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   61 SEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITF 120
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APPLICANT: Hakee, David
APPLICANT: Hakee, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REFERENCE: 2002-10-31
CURRENT FILING DATE: 2002-10-31
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-110-10
PRIOR PILING DATE: 2001-110-19
PRIOR PILING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
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PRIOR PILING DATE: 2002-10-39
PRIOR PILING DATE: 2002-10-39
PRIOR PILING DATE: 2002-10-39
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-05
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-08-16
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PRIOR PILING DATE: 2002-08-18
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Sequence 10, Application PC/TUS0234502

Sequence 10, Application PC/TUS0234502

GENERAL INFORMATION:
APPLICANT: ZymoGenetics, Inc.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37PC
CURRENT APPLICATION NUMBER: PCT/US02/34502
                                                          KSFKKNLKDFLFEIPFDCWKPAQK 144
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Neose Technologies, I
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, Caryn
APPLICANT: Chen, Xi
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Best Local Similarity 76.4*
Matches 110; Conservative
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ORGANISM: Homo sapiens
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Search completed: May 25, 2006, 15:12:38 Job time : 601 secs

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Sequence 541, App
Sequence 447, App
Sequence 440, App
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Sequence 448, App
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Sequence 541, App
Sequence 324, App
Sequence 324, App
Sequence 324, App
Sequence 324, App
Sequence 322, App
Sequence 232, App
Sequence 232, App
Sequence 232, App
Sequence 232, App
Sequence 231, App
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157.333 Million cell updates/sec
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Sequence 540,
Sequence 541,
Sequence 447,
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/EMC_Celerra_SIDS3/ptodata/2/paa/US06_NEW_COMB.pep:*
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/EMC_Celerra_SIDS3/ptodata/2/paa/US11_NEW_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/paa/US11_NEW_COMB.pep:*
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GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                      May 25, 2006, 15:02:47; Search time 19 Seconds
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US-11-429-374-448
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Listing first 45 summaries
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Match Length
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Sequence 15, Appl Sequence 9903, Ap	Sequence 25484, A Sequence 17334, A		Sequence 18035, A Sequence 22443, A		Sequence 11908, A		Sequence 23006, A	'n	Sequence 19633, A	Sequence 52, Appl	Sequence 30773, A	Seguence 10487, A	Seguence 25602, A
US-11-326-710-15 US-11-431-855-9903 US-11-431-855-19139	US-11-431-855-25484 US-11-431-855-17334	US-11-431-855-436 US-11-431-855-14091	US-11-431-855-18035 US-11-431-855-22443	US-11-431-855-12223	US-11-431-855-11908	US-11-431-855-29329	US-11-431-855-23006	US-11-431-855-32535	US-11-431-855-19633	US-10-966-645A-52	US-11-431-855-30773	US-11-431-855-10487	US-11-431-855-25602
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                                                                                    APPLICANT: ROSEN et al.

TITLE OF INVENTION: Albumin Fusion Proteins
FILIS REPERENCE: PF564

CURRENT APPLICATION NUMBER: US/11/429,373

CURRENT FILING DATE: 2006-05-08

PRIOR PILING DATE: 2004-02-12-23

PRIOR FILING DATE: 2002-12-23

PRIOR PILING DATE: 2002-12-23

PRIOR PILING DATE: 2002-12-23

PRIOR PILING DATE: 2002-12-23

PRIOR PILING DATE: 2002-02-28

PRIOR PILING DATE: 2002-02-28

PRIOR PILING DATE: 2002-05-10

PRIOR PILING DATE: 2002-05-10

PRIOR PLING DATE: 2002-05-10

PRIOR PLING DATE: 2002-05-10

PRIOR PLING DATE: 2002-05-10

PRIOR PLING DATE: 2002-05-10

PRIOR PILING DATE: 2002-09-18

PRIOR PILING DATE: 2002-10-11

PRIOR PLING DATE: 2002-10-23

REMAINING PAPLICATION NUMBER: 60/417,611

PRIOR PLING DATE: 2002-10-13

PRIOR PLING DATE: 2002-10-13

PRIOR PLING DATE: 2002-10-23

REMAINING PRIOR APPLICATION NUMBER: 60/410,611

PRIOR PLING DATE: 2002-10-13

PRIOR PLING DATE: 2002-10-23

REMAINING PLING DATE: 2002-10-23

SOFTWARE: PRIOR APPLICATION NUMBER: 60/410,611

PRIOR PLING DATE: 2002-10-13

PRIOR PLING DATE: 2002-10-13

PRIOR PLING DATE: 2002-10-11

PRIOR PLING DATE: 2002-10-13

PRIOR PLING DATE: 2002-10-23

SOFTWARE: PRIOR APPLICATION NUMBER: 60/410,420,464

PRIOR PLING DATE: 2002-10-23

SOFTWARE: PRIOR APPLICATION NUMBER: 60/410,420,464

PRIOR PLING DATE: 2002-10-23

SOFTWARE: PRIOR APPLICATION NUMBER: 60/410,420,464

PRIOR PLING DATE: 2002-10-23

PRIOR PLING DATE: 2002-10-23

PRIOR PLING DATE: 2002-10-23
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                   Sequence 447, Application US/11429373
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 76.4
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-11-429-373-447
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61 SETFDAEELTCLOTRLKLYKOGLRGSLIKLEGPLTMMASHYKOHCPPTLETSCATOMITF 120
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              FRIOR AFFILLALIAN NUMBER: 60/341,811

PRIOR APPLICATION NUMBER: 60/341,811

PRIOR APPLICATION NUMBER: 60/340,000

PRIOR APPLICATION NUMBER: 60/360,000

PRIOR PILING DATE: 2001-12-21

PRIOR PILING DATE: 2002-02-80

PRIOR PILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: 60/338,008

PRIOR APPLICATION NUMBER: 60/411,355

PRIOR FILING DATE: 2002-07-24

PRIOR FILING DATE: 2002-09-18

PRIOR PILING DATE: 2002-09-18

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2002-10-10

PRIOR PILING DATE: 2002-10-10

PRIOR PRIOR PILING DATE: 2002-10-10

PRIOR PILING DATE: 2002-10-10

PRIOR PILING DATE: 2002-10-13

PRIOR PILING DATE: 2002-10-23

REMBARING PRIOR APPLICATION NUMBER: 60/420,246

PRIOR PILING DATE: 2002-10-23

REMBARING PRIOR APPLICATION NUMBER: 2002-10-23

REMBARING PRIOR APPLICATION NUMBER: 2002-10-23

REMBARING PRIOR APPLICATION NUMBER: 00/420,246

PRIOR PILING DATE: 2002-10-23

REMBARING PRIOR APPLICATION NUMBER: 2002-10-23

REMBARING PRIOR PRIOR APPLICATION NUMBER: PARCHER PRIOR PALM.
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Sequence 541, Application US/11429373
GENERAL INFORMATION:
PAPPLICANT: Rosen et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PFS64
CURRENT APPLICATION NUMBER: US/11/429,373
CURRENT FILING DATE: 2006-05-08
PRIOR APPLICATION NUMBER: 10/775,204
PRIOR APPLICATION NUMBER: PCI/USO2/40891
PRIOR FILING DATE: 2002-12-23
PRIOR FILING DATE: 2002-12-23
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-8
PRIOR FILING DATE: 2002-02-8
PRIOR FILING DATE: 2002-03-8
PRIOR FILING DATE: 2002-03-18
PRIOR FILING DATE: 2002-03-18
PRIOR FILING DATE: 2002-01-8
PRIOR FILING DATE: 2002-01-8
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
PRIOR PILING DATE: 2002-10-13
PRIOR PILING DATE: 2002-10-13
APPLICATION NUMBER: PCT/US02/40891
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ORGANISM: Homo sapiens
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       61 SEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTWMASHYKQHCPPTPETSCATQIITF 120
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Albumin Fusion Proteins

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REPERENCE: PF564

CURRENT APPLICATION NUMBER: US/11/429,373

CURRENT FILING DATE: 2006-05-08

FRIOR APPLICATION NUMBER: 10/775,204

FRIOR APPLICATION NUMBER: 60/341,811

FRIOR PILING DATE: 2002-12-23

FRIOR APPLICATION NUMBER: 60/340,000

FRIOR PILING DATE: 2002-02-28

FRIOR APPLICATION NUMBER: 60/378,950

FRIOR FILING DATE: 2002-02-26

FRIOR APPLICATION NUMBER: 60/411,355

FRIOR FILING DATE: 2002-07-64

FRIOR FILING DATE: 2002-07-64

FRIOR FILING DATE: 2002-07-64

FRIOR FILING DATE: 2002-07-64

FRIOR PELING DATE: 2002-07-64

FRIOR PELING DATE: 2002-07-64

FRIOR PELING DATE: 2002-07-16

FRIOR PELING DATE: 2002-10-02

FRIOR FILING DATE: 2002-10-10-03

FRIOR FILING DATE: 2002-10-10-03

FRIOR FILING DATE: 2002-10-03

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 540, Application US/11429373
Sequence 540, Application US/11429373
GENERAL INFORMATION:
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION WHERE: US/11/429,373
CURRENT FILING DATE: 2006-05-08
PRIOR APPLICATION WHERE: 10/775,204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFKENLKDFLLVIPFDCWEPVQE 144
                                                                                                                121 KSFKKNLKDFLFEIPFDCWKPAQK 144
                                                                         KSFKKNLKDFLFEIPFDCWKPAQK 144
                                                                                                                                                                                                                                                                           US-11-429-373-448; Sequence 448, Application US/11429373; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.4%
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-11-429-373-448
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US-11-429-373-540
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61 SETFDABELTCLOTRLKLYKOGLRGSLIKLEGPLTMMASHYKOHCPPTLETSCATOMITF 120
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TITLE OF INVENTION: Albumin Fusion Proteins
TITLE REFERENCE: PF564
CURRENT APPLICATION WUMBER: US/11/429,374
CURRENT APPLICATION NUMBER: US/11/429,374
CURRENT FILING DATE: 2004-02-11
FRIOR APPLICATION NUMBER: 10/775,204
FRIOR APPLICATION NUMBER: 00/341,811
FRIOR APPLICATION NUMBER: 60/341,811
FRIOR APPLICATION NUMBER: 60/360,000
FRIOR TLING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: 60/378,950
FRIOR APPLICATION NUMBER: 60/378,950
FRIOR APPLICATION NUMBER: 60/411,355
FRIOR APPLICATION NUMBER: 60/411,355
FRIOR FILING DATE: 2002-07-01-8
FRIOR PILING DATE: 2002-07-01-8
FRIOR PILING DATE: 2002-07-01-8
FRIOR APPLICATION NUMBER: 60/411,355
FRIOR APPLICATION NUMBER: 60/411,611
FRIOR APPLICATION NUMBER: 60/414,984
FRIOR APPLICATION NUMBER: 60/414,984
FRIOR FILING DATE: 2002-10-02
FRIOR FILING DATE: 2002-10-10-23
FRIOR FILING DATE: 2002-10-23
FRIOR FILING DATE: 2002-10-23
FRIOR FILING DATE: 2002-10-23
FRIOR FILING DATE: 2002-10-23
FRIOR APPLICATION NUMBER: 60/420,246
FRIOR FILING DATE: 2002-10-23
FRIOR APPLICATION NUMBER: 60/420,246
FRIOR FILING DATE: 2002-10-23
FRIOR APPLICATION NUMBER: 60/420,246
FRIOR FILING DATE: 2002-10-23
FRIOR APPLICATION NUMBER: 60/420,246
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FRIOR APPLICATION NUMBER: 60/420,246
FRIOR FILING DATE: 2002-10-23
FRIOR APPLICATION NUMBER: 60/420,246
FRIOR FILING DATE: 2002-10-23
FRIOR APPLICATION NUMBER: 60/420,246
FRIOR FILING DATE: 2002-10-23
FROM FRIOR FILING DATE: 2002-10-23
FROM FROM FILING DATE: 2002-10-23
FROM FROM FILING DATE: 2002-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 540, Application US/11429374
GENERAL INFORMATION:
APPLICANT ROSEN et al.
TITLE OF INVENTION: Albumin Fusion Proteins;
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/11/429,374
CURRENT FILING DATE: 2006-05-08
PRIOR APPLICATION NUMBER: 10/775,204
                                                                                                                                                                  121 KSFKKNLKDFLFEIPFDCWKPAQK 144
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ESFKENLKDFLLVIPFDCWEPVQE 144
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; Sequence 448, Application US/11429374
; GENERAL INFORMATION:
                                                                                                                       121 KSFKKNLKDFLFEIPFDCWKPAQK
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SEMPDLQEPTCLQTRLELYKQGLRGSLTXLKGPLTMMASHYKQHCPPTPETSCATQLITF 120
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/11/429,374
CURRENT FILING DATE: 2006-05-08
FRIOR PEDICATION NUMBER: 10/775,204
FRIOR PELING DATE: 2004-02-11
FRIOR APPLICATION NUMBER: PCT/US02/40891
FRIOR APPLICATION NUMBER: PCT/US02/40891
FRIOR APPLICATION NUMBER: PCJ/341,811
FRIOR APPLICATION NUMBER: 60/341,811
FRIOR APPLICATION NUMBER: 60/340,000
FRIOR FILING DATE: 2002-02-29
FRIOR PELING DATE: 2002-02-24
FRIOR APPLICATION NUMBER: 60/398,008
FRIOR APPLICATION NUMBER: 60/398,008
FRIOR PELING DATE: 2002-07-24
FRIOR FILING DATE: 2002-07-24
FRIOR FILING DATE: 2002-10-02
FRIOR FILING DATE: 2002-10-02
FRIOR APPLICATION NUMBER: 60/417,611
FRIOR APPLICATION NUMBER: 60/417,611
FRIOR APPLICATION NUMBER: 60/417,611
FRIOR PELING DATE: 2002-10-11
FRIOR PELING DATE: 2002-10-11
FRIOR FILING DATE: 2002-10-11
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   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
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SEQ ID NO 447
LENGTH: 144
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Matches 110; Conservative
                                                                                                                                                                                          TYPE: PRT CORGANISM: Homo sapiens US-11-429-373-541
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US-11-429-374-447
                                                                                                               SEQ ID NO 541
LENGTH: 144
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PRIOR FILING DATE: 2002-10-23
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 540
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CURRENT APPLICATION NUMBER: US/11/429,374
CURRENT FILING DATE: 2006-05-08
RIOR APPLICATION NUMBER: US/775,204
PRIOR FILING DATE: 2004-02-11
PRIOR PILING DATE: 2004-02-11
PRIOR FILING DATE: 2002-12-3
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR APPLICATION NUMBER: 60/340,000
PRIOR APPLICATION NUMBER: 60/340,000
PRIOR FILING DATE: 2002-02-8
PRIOR FILING DATE: 2002-02-8
PRIOR PELING DATE: 2002-03-10
PRIOR FILING DATE: 2002-03-10
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-18
PRIOR FILING DATE: 2002-09-18
PRIOR PELING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR PELING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/411,515
PRIOR PELING DATE: 2002-10-12
PRIOR PELING DATE: 2002-10-11
PRIOR PELING DATE: 2002-10-11
PRIOR PELING DATE: 2002-10-11
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: PCT/US02/40891
PRIOR PILING DATE: 2002-12-3
PRIOR PELICATION NUMBER: 60/341,811
PRIOR PELICATION NUMBER: 60/341,811
PRIOR PELICATION NUMBER: 60/360,000
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/318,008
PRIOR PILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-02
PRIOR PELING DATE: 2002-10-02
PRIOR PELING DATE: 2002-10-02
PRIOR PELING DATE: 2002-10-11
PRIOR PELING DATE: 2002-10-11
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ESFKENLKDFLLVIPFDCWEPVQE 144
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Homo sapiens
US-11-429-374.540
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FILE KEREMENCE: P5.64

CURRENT FILING DATE: 2006-05-08

PRIOR PLILAGION NUMBER: 10/775,204

PRIOR PLILAGION NUMBER: 10/775,204

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PRIOR PLING DATE: 2004-02-11

PRIOR PLING DATE: 2002-12-23

PRIOR PLING DATE: 2001-12-21

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PRIOR PLING DATE: 2001-12-21

PRIOR PLING DATE: 2001-12-21

PRIOR PLING DATE: 2002-02-8

PRIOR PLING DATE: 2002-02-8

PRIOR PLING DATE: 2002-05-10

PRIOR PLING DATE: 2002-05-10

PRIOR PLING DATE: 2002-05-10

PRIOR PLING DATE: 2002-09-18

PRIOR PLING DATE: 2002-10-11

PRIOR PLING DATE: 2002-10-23

PRIOR PLING DATE: 2002-10-11

PRIOR PLING DATE: 2002-10-23

PRIOR PLING DATE: 2002-10-11

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Remaining Prior Application data removed · See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 541
LENGTH: 144
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
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Matches 110; Conservative
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Matches 110; Conservative
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ORGANISM: Homo sapiens
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US-11-429-374-541
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US-11-429-276-541
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                                     61 SEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPFTPETSCATQIITF 120
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TITLE OF INVENTION: Albumin Fusion Proceins
TITLE OF INVENTION: Albumin Fusion Proceins
CURRENT APPLICATION NUMBER: US/11/429,276
CURRENT APPLICATION NUMBER: 10/775,204
PRIOR PELICATION NUMBER: 10/775,204
PRIOR PELICATION NUMBER: PCT/US02/40891
PRIOR PELING DATE: 2004-02-11
PRIOR PELING DATE: 2004-02-11
PRIOR PELING DATE: 2001-12-21
PRIOR PELING DATE: 2001-12-21
PRIOR PELING DATE: 2002-02-28
PRIOR PELING DATE: 2002-05-29
PRIOR PELING DATE: 2002-05-10
PRIOR PELING DATE: 2002-05-10
PRIOR PELING DATE: 2002-05-10
PRIOR PELING DATE: 2002-05-10
PRIOR PELING DATE: 2002-01-29
PRIOR PELING DATE: 2002-01-29
PRIOR PELING DATE: 2002-10-02
PRIOR PELING DATE: 2002-10-02
PRIOR PELING DATE: 2002-10-03
PRIOR PELING DATE: 2002-10-03
PRIOR PELING DATE: 2002-10-03
PRIOR PELING DATE: 2002-10-11
PRIOR PELING DATE: 2002-10-13
PRIOR PELING DATE: 2002-10-03
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/11/429,276
CURRENT FILING DATE: 2006-05-08
                                                                                                                                                              121 KSFKKNLKDFLFEIPFDCWKPAQK 144
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US-11-429-276-448
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US-11-429-276-448
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61 SETFDAEELTCLOTRLKLYKQGLRGSLIKLEGPLTWMASHYKQHCPPTLETSCATQMITF 120
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PRIOR PILING DATE: 2004-02-11

PRIOR PLING DATE: 2004-02-12-3

PRIOR FILING DATE: 2004-02-12-3

PRIOR FILING DATE: 2001-12-21

PRIOR PLICATION NUMBER: 60/341,811

PRIOR PLICATION NUMBER: 60/360,000

PRIOR PILING DATE: 2002-03-0

PRIOR PILING DATE: 2002-05-10

PRIOR PILING DATE: 2002-05-10

PRIOR PILING DATE: 2002-05-10

PRIOR PILING DATE: 2002-05-10

PRIOR PILING DATE: 2002-0-18

PRIOR PILING DATE: 2002-0-18

PRIOR PLING DATE: 2002-0-18

PRIOR PLING DATE: 2002-10-02

PRIOR PLING DATE: 2002-10-11

PRIOR PLICATION NUMBER: 60/414,984

PRIOR PLING DATE: 2002-10-11

PRIOR PLING DATE: 2002-10-21

PRIOR PLING DATE: 2002-10-21

PRIOR PLING DATE: 2002-10-11

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PRIOR PLING DATE: 2002-10-10

PRIOR PLING DATE: 2002-10-11

PRIOR PLING DATE: 2002-10-21

PRIOR PLING DATE: 2002-10-23

SOFTWARE: PALENTIN Ver. 2.0

SEQ ID NOS: 2222

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CURRENT APPLICATION NUMBER: US/11/429,276
CURRENT FILING DATE: 2006-05-08
PRIOR FILING DATE: 2006-05-11
PRIOR FILING DATE: 2004-02-11
PRIOR PELING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: PCT/US02/40891
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2001-12-21
PRIOR PELING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR PILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR PILING DATE: 2002-07-24
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR APPLICATION NUMBER: 60/411,551
PRIOR APPLICATION NUMBER: 60/411,515
PRIOR APPLICATION NUMBER: 60/411,611
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
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Best Local Similarity 76.4%
Matches 110; Conservative
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ORGANISM: Homo sapiens
US-11-429-276-540
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US-11-429-276-324
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Albumin Fusion Proteins

TITLE OF INVENTION: Albumin Fusion Proteins

TITLE OF INVENTION: Albumin Fusion Proteins

CURRENT APPLICATION NUMBER: US/11/429,373

CURRENT FILING DATE: 2006-05-08

PRIOR APPLICATION NUMBER: 0/341,811

PRIOR APPLICATION NUMBER: 60/341,811

PRIOR APPLICATION NUMBER: 60/341,811

PRIOR APPLICATION NUMBER: 60/340,000

PRIOR FILING DATE: 2002-02-28

PRIOR PILING DATE: 2002-05-10

PRIOR PILING DATE: 2002-05-10

PRIOR FILING DATE: 2002-07-44

PRIOR PILING DATE: 2002-07-44

PRIOR APPLICATION NUMBER: 60/411,355

PRIOR PILING DATE: 2002-07-10-24

PRIOR PILING DATE: 2002-01-02

PRIOR PILING DATE: 2002-01-02

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-03

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-03

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2222

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PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ 1D NOS: 222
SOFTWARE: Patentin Ver. 2.0
SEQ 1D NO 541
LENGTH: 144
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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FILER REPERENCE: PPS64
CURRENT APPLICATION NUMBER: US/11/429,374
CURRENT FILING DATE: 2006-05-08
PRIOR PELING DATE: 2006-05-08
PRIOR PELING DATE: 2004-02-11
PRIOR PILING DATE: 2002-02-11
PRIOR FILING DATE: 2002-12-13
PRIOR PILING DATE: 2002-12-23
PRIOR PILING DATE: 2002-12-21
PRIOR PILING DATE: 2002-02-28
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PRIOR PILING DATE: 2002-05-18
PRIOR PILING DATE: 2002-05-18
PRIOR PILING DATE: 2002-05-18
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR APPLICATION NUMBER: 60/411,611
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR PILING DATE: 2002-10-11
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/11/429,276
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Matches 110; Conservative
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ORGANISM: Homo sapiens
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CUKKENT FILING DATE: 2006-05-08

PRIOR APPLICATION NUMBER: 10/775,204

PRIOR FILING DATE: 2004-02-11

PRIOR FILING DATE: 2004-02-11

PRIOR PELICATION NUMBER: PCT/US02/40891

PRIOR PELICATION NUMBER: 60/341,811

PRIOR FILING DATE: 2002-12-23

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-07-24

PRIOR PELICATION NUMBER: 60/491,355

PRIOR PELICATION NUMBER: 60/411,355

PRIOR PELICATION NUMBER: 60/411,355

PRIOR PELICATION NUMBER: 60/411,611

PRIOR PELING DATE: 2002-10-01

PRIOR PELING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: 60/417,611

PRIOR APPLICATION NUMBER: 60/410,611

PRIOR PELING DATE: 2002-10-02

PRIOR PELING DATE: 2002-10-23

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2222

SOFTWARE: PALENTIN VER. 2002-10-3

SEQ ID NO 324

TYPE: PDATE: 2003-10-3

TYPE: PORTAL TOPE: PORTAL TOPE: 2003-10-3

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; ORGANISM: Homo sapiens
US-11-429-276-324
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Bublot,M., Perez,J.M. and Andreoni,C.M.P.
Nucleic acids encodings equine GM-CSF
Patent: US 6645740-A 8 11-NOV-2003;
Merial Limited and Merial LLC; London;
GBX;
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100.0%; Pred. No. 9e-105;
ive 0; Mismatches 0;
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Sequence 8 from patent US 6645740.
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Matches 435; Conservative
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TITLE
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AY040203 Equus cab
AX040203 Equus cab
AX53561 Ovine GM-CS
DO010419 Capra hir
X53561 Ovine GM-CS
DO110419 Cervus elap
D21074 Sus scrofa
AX067831 Sequence
U67175 Sus scrofa
BD211588 Canine an
BD211588 Canine an
AR241565 Sequence
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                   GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
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AF448481 AM 12-AUG-2002 Equus caballus granulocyte-macrophage colony-stimulating factor (GM-CSF) mRNA, partial cds.
AF4448481.2 GI:22208937
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Equidae; Equus.
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                                                                                                                                                           Equus sp.
Equus sp.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Laurasiatheria; Perissodactyla;
                                                                                                                                                                                                                          Fischer, L.J., barzu-le Roux, S. and Audonnet, J.C. Dna vaccines for pets and sport animals Patent: WO 0077043-A 69 21-DEC-2000; MERIAL (FR)
                                                                                           DNA
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/organism="Equus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:46122"
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Sequence 69 from Patent WO0077043.
AX067832 AX067832.1 GI:12329710
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Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus
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Equine granulocyte-macrophage colony-stimulating factor (gm-csf)
Patent: WO 0077210-A 8 21-DEC-2000;
MERIAL (FR)
                                                                 TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAA
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100.0%; Score 435; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 9e-105;
Matches 435; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      linear
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    .435
    /organism="Equus sp."
    /mol_type="unassigned DNA"
    /db_xref="taxon:46122"

                                                                                                                                                                                                                                                                      AX057390 435 bp
Sequence 8 from Patent WO0077210.
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Eguus sp.
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	779 bp mRNA linear 11ocyte-macrophage colony-stimula 1al cds. 1524	CE RS CE CE	Direct Sub Submitted Koenigin-I 3 (bases Mauel, S., Direct Sub Submitted Koenigin-I	REMARK Sequence update by submitter  COMMENT On Nov 5, 2001 this sequence version replaced gi:14764537.  FRATURES 1. 779  Source /organism="Equus caballus"  /mol type="memory" / db xref="taxon:9756"  /cell type="ConA activated PBMC"	V - V - 8 V 4 8 M	/db_xref="G1:15740E55" //tb_xref="G1:15740E55" //translation="MMLQNLLLLGTVVSMPAPTRQPSPVTRPWQHVDAIKEALSLLN NSSDTAALMNETVEVVSETPDAEGTCLQTRAKLYRQGLRGSLIKLEGPLTMASHYK QHCPPTLETSCATQMITFKSFKRNLKDFLFEIPFDCWNQPRSKAGLPARS"  Query Match 96.5%; Score 419.8; DB 14; Length 779; Best Local Similarity 99.3%; Pred. No. 1.1e-100; Matches 432; Conservative 0; Mismatches 2; Indels 1; Gaps 1; Qy 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGGTTTACAGCATGCCCGCACC Db 1 ATGTGGCTTGCAACCTGGTCTTTTTTTTTTTTTTTTTTT
SOURCE SQUES Equus caballus (horse) ORGANISM Equus caballus (horse) ORGANISM Equus caballus (horse) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lo 438) AUTHORS Vecchione, A., D'Mello, F., Kanellos, T.S., Howard, C.R., Hamblin, A.S. and Catchpole, B. TITLE JOURNAL Unpublished REFERENCE 2 (bases 1 to 438) AUTHORS Vecchione, A., D'Mello, F., Kanellos, T.S., Howard, C.R., Hamblin, A.S.	TITLE Direct Submission JOURNAL Submitted (16-NOV-2001) Department of Pathology and Infectious JOURNAL Submitted (16-NOV-2001) Department of Pathology and Infectious Diseases, Royal Veterinary College, Royal College Street, London NW1 OTU, UK REFERENCE 3 (bases 1 to 438) AUTHORS Vecchione, A., D'Mello, F., Kanellos, T.S., Howard, C.R., Hamblin, A.S. and Catchpole, B. TITLE Direct Submission JOURNAL Submitted (12-AUG-2002) Department of Pathology and Infectious Diseases, Royal Veterinary College, Royal College Street, London	NW1 0TU, UK  REMARK Sequence update by submitter  COMMENT On Aug 12, 2002 this sequence version replaced gi:17646732.  FEATURES Location/Qualifiers  SOUTCE 1. 438  /mol type="MRNA" /mol type="MRNA" /db Xref="taxon:9796" /coll type="cond-activated PBMC"	marrow progenitor cell	/product="granulocyte-macrophage colony-stii factor" /protein id="AAL41017.2" /db_xref="G1:22208938" /translation="WMLQNLLLGTVVYSMPAPTRQPSPVTRP NSSDTAAIMNETVEVVSETFDAEELTCLGTRLKLYKQGLRGSL QHCPPTLETSCATQMITFKSFKKNLKDFLFEIPFDCWKPAQKLI	Query Match 99.3%; Score 432; DB 14; Length 438; Best Local Similarity 100.0%; Pred. No. 5.6e-104; Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGCTTTACAGCATGCCCGCACCCACC	

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DQ010419 435 bp mRNA linear MAM 26-APR-2005 Capra hircus granulocyte-macrophage colony stimulating factor (GM-CSF) mRNA, complete cds.
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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Peccra; Boyidae; Caprine; Capra.

S Shu,D.Q., Cao,S.X., Mao,D.G., Wu,Z.M. and Yang,L.G.

Cloning and Sequence Analysis of Capra Hircus

Granulocyte-macrophage Colony Stimulating Factor (GM-CSF)

Unpublished

2 (bases 1 to 435)

S Shu,D.Q., Cao,S.X., Mao,D.G., Wu,Z.M. and Yang,L.G.

Direct Submission

L Submitted (18-APR-2005) The Animal Breed Institute, Nanjing Agricultural University, Nanjing, Jiangeu 210095, China

Location/Qualifiers
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Pred. No. 1.2e-85;
0; Mismatches 43; Indels
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/organism="Capra hircus"
/mol_type="mRNA"
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1. .435
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/gene="GM-CSF"
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Best Local Similarity
Matches 389; Conserv
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Submitted (12-OCT-1990) O'Brien P., Commonwealth Scientific &
Industrial Research, (CSIRO) Division of Animal Health, Private Bag
No 1, Parkville Vic 3052, Australia
Stimulates bone marrow progenitor cells to proliferate and
differentiate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /procein_id="CAA39463.1"
/boxeein_id="CAA39463.1"
/db_xref="GOA:Q9MXK4"
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DSTDTPAAVMDETVEWEMFDSQEPTCLQTRLELYKQGLRGSLTGSLTGSLTWMASHYK
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Ovine GM-CSF mRNA for granulocyte-macrophage colony stimulating
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Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
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    .432
/product="granulocyte-macrophage colony-stimulating

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|product="granulocyte-macrophage_colony-stimulating
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cytokine; granulocyte-macrophage colony stimulating factor.
Ovis aries (sheep)
Ovis aries
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/organism="Ovis aries"
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COMMENT

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type="mRNA"
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                                  /protein_id="AAY16326.1"
/db_xref="G1:6282818"
/translation="MMLQNLLLGTVVCSFSAPTRQPSPVTWPWQHVDAIKEALSLLN
DSSDTAAVMMETVEWVSEMPDSQEPTCLQTRLELYRQGLRGSLTSLTGSLTMMASHYK
KYCPPTQETSCETQIITFKSFKENLKDPLFIIPFDCWRPPVQK"
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X53561
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Submitted (20-JUN-1990) McInnes C.J., Moredum Research Institute,
408 Gilmerton Rd., Edinburgh EH17 7JH, Scotland, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            granulocyte-macrophage colony stimulating factor; signal peptide.
Ovis aries (sheep)
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           'product="granulocyte-macrophage colony stimulating
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Cloning and expression of a cDNA encoding ovine
granulocyte-macrophage colony-stimulating factor
Gene 105 (2), 275-279 (1991)
                                                                                                                         Score 363; DB 14;
Pred. No. 1.3e-85;
0; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Laurasiathe
Pecora; Bovidae; Caprinae; Ovis
 codon start=1
                                                                                                                         83.4%;
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McInnes, C.J.
                                                                                                                                      Best Local Similarity 89.7
Matches 390, Conservative
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/organism="Ovis aries"

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41. .3496
42. .3496
43. .448
6codon start=1
6producT= GAM-CSF precursor"
6producT= GAM-CSF precursor"
6producT= GAM-CSF precursor"
6protein id="CAA37632.1"
6protein id="CAA3763"
6protein 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Cervidae; Cervinae; Cervus.
1 (bases 1 to 432)
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Cervus elaphus granulocyte-macrophage colony-stimulating factor
(GM-CSF) mRNA, partial cds.
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83.4%; Score 363; DB 14; Length 495;
Best Local Similarity 89.7%; Pred. No. 1.4e-85;
Matches 390; Conservative 0; Mismatches 45; Indels
/isolate="pGMCSF22"
/db_xref="taxon:9940"
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/product="GM-CSF"
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/protein_id="BAA04649.1"
                                                                                                                                                                                                                                                                                      organism="Sus scrofa"
                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9823"
/clone="pPGM"
                                                                                                             Inumaru, S. and Takamatsu, H.
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/cell_tvpe="T
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            GI:497829
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Matches 372; Conservative
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HSSDTAAVMNETVEVVSEMFDSQEPTCLQTRLKLYKQGLRGSLTSLSGSLTMMARHYE
QHCPPTQETSCETQTITFKSFKENLKDFLFIIPFDCWEPAQK"
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                                                 Direct Submission
Submitted (05-SEP-1994) Euan A Lockhart, Microbiology, Deer
Research Laboratory, University of Otago, Union St., Dunedin, New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGAAATGTTTGACTCCCAGGAGCCGACATGCCTGCAGACTCGCCTGAAGCTGTACAAG
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gene="GM-CSF"
Codon start=1
product="granulocyte-macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                       Score 358.4; DB 14; Length 432; Pred. No. 2.2e-84; 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIGGMCSF 435 bp mRNA linear Sus scrofa GM-CSF mRNA for granulocyte-macrophage colony-stimulating factor, complete cds.
  cervine GM-CSF
                                                                                                                          organism="Cervus elaphus"
                                                                                                                                                                                                                                                    protein_id="AAA21439.1"
                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9860"
                                                                                                                                                                                                                                                                                                                           /note="PCR primer"
complement(413, .432)
/note="PCR primer"
                                                                                                                                                                                                                                                                 db xref="GI:537896"
                                                                                                   Location/Qualifiers
Cloning and sequencing of Unpublished 2 (bases 1 to 432) Lockhart, E.A.
                                                                                                                                                                            'gene="GM-CSF"
                                                                                                                                                                                                                                                                                                                                                                                         82.4%;
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                                                                                                                                                                 .432
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PIGGMCSF
  TITLE
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REFERENCE
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                                        AUTHORS
                                                                JOURNAL
                                                                                                                                                                                       CDS
                                                                                                   FEATURES
                                                     TITLE
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/db_xref="G1:497830"
ft=anslation="wmuQNULLIGTVVCSISAPTRPPSPVTRPWQHVDAIKEALSLLN
NSNDTAAVMMETVDIVCEMEDPQEPCVQTRLNLYRQGLRGSLTRLKSPLTLLAKHYE
QHCPLTBETSCETQSITFKSPKD&LNKFLFTIPFDCWEPAQK"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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                                                                                                                                            colony-stimulating
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1. .435
/inference="non-experimental evidence, no additional details recorded"
/note="GM-CSF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (06-OCT-1993) Shigeki Inumaru, National Institute chamitted (06-OCT-1993) Shigeki Inumaru, National Institute chaminal Health, Biological Products Research Division; 3-1-1, Kannondai, Tsukuba, Ibaraki 305, Japan (Tel:81-298-38-8624, Fax:81-298-38-7880)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="granulocyte-macrophage colony-stimulating
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                                                                                                                                            cDNA cloning of porcine granulocyte-macrophage
                                                                                                                                                                                               (5), 474-476 (1995)
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/db xref="G1:1513128"
/translation="MWLQNLLLLGGTVVCSISAPTRPPSPVTRPWQHVDAIKEALSLLN
NSNDTAAVMNETVDVVCEMFDPQEPTCVQTRLNLYKQGLRGSLTRLKSPLTLLAKHYE
QHCPLTEETSCETQSITFKSFKDSLNKFLFTIPFDCWGPVKK"
                                                                                                                                                          To bases 1 to 435)
Gloster, S.E., Sandeman, R.M. and Strom, A.D.G.
Gloster, S.E., Sandeman, R.M. and Strom, A.D.G.
Cloning of a cDNA and gene encoding porcine granulocyte macrophage-
colony stimulating factor (GM-CSF)
Unpublished
Glassel to 435)
Gloster, S.E., Sandeman, R.M. and Strom, A.D.G.
Direct Submission
Submitted (19-MG-1996) Animal Health, CSIRO, Park Drive,
Melbourne, VIC 3052, Australia
Location/Qualifiers
                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCATGCATGCCATCAAGGAGGCCCTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .20
/note="based on the porcine genomic DNA sequence"
complement (416. .415)
/note="based on the porcine genomic DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ell type="alveolar macrophages".435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_id="AAB06854.1"
                                                                                                                                                                                                                                                                                                                                                                                      1. 435
/organism="Sus scrofa"
/nol_type="mRNA"
/db_xref="taxon:9823"
/cell_type="alveolar mac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="cytokine"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="GM-CSF"
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                     GI:1513327
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Matches 371; Conservative
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                                                             Sus scrofa (pig)
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                                                                                                                                                                                   PAT 19-JAN-2001
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSU67175 435 bp mRNA linear MAM 30-AUG-1996 Sus scrofa granulocyte macrophage-colony stimulating factor (GM-CSF) mRNA, complete cds.
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                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                       Fischer, L.J., barzu-le Roux, S. and Audonnet, J.C. Dna vaccines for pets and sport animals Patent: WO 0077043-A 68 21-DEC-2000; MERIAL (FR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 332.6; DB :
Pred. No. 1.6e-77
                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches

    .435
    /organism="Felis catus"
/mol_type="unassigned DNA"
/db_xref="taxon:9685"

                                                                                                                                                                               AX067831 435 bp
Sequence 68 from Patent WO0077043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                             AX067831.1 GI:12329709
                                      CCAGCCCAGAAGTAA 435
                                                             CCAGCCCAGAAGTGA 435
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Best Local Similarity
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AUTHORS Sim, G., Yang, S., Dreitz, M.J. and Wonderling, R.S.

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TOURNAL PETENT: UP 2002516104-A 94 04-UUN-2002;

FNT BY 2002516104-A/94

PN JP 2002516104-A/94

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CEKKEE SIM.SHUMIN VAATHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
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/mol_type="genomic DNA"
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[ Labases 1 to 444)

Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.

Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
Patent: JP 2002516104-A 93 04-JUN-2002;
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/mol_type="genomic DNA"
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                                                                    TACAAGCAGCACTGCCCCCCCCCAGGAAACTTCCTGTGCAACCCAGATGATCACCTTC 360
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                              TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAA
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Unclassified.
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Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
Canine IL-4 immunoregulatory proteins and uses thereof
Patent: US 6471957-A 119 29-OCT-2002;
Heska Corporation; Fort Collins, CO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.5%; Score 332.6; DB 2; Length 444; 85.3%; Pred. No. 1.6e-77; Ative 0; Mismatches 64; Indels 0;
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Sequence 119 from patent US 6471957.
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/organism="unknown"
/mol_type="genomic DNA"
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completed: May 26, 2006, 01:32:18

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Aaf55040 Nucleotid
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                            The invention relates to a novel DNA vaccine against pathogens that affect pets and sports animals comprises a plasmid containing a sequence, expressible in vivo, that encodes an immunogen from the relevant pathogen and a cationic lipid containing a quaternary ammonium salt, particularly N-(2-hydroxypethyl)-N-M-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium (DMRIE). The immunogens are particularly taken from canine distemper virus (CHV), canine parainfiluenza virus type 1 (FHV-1), equine herpes virus type 1 (EHV-1), equine herpes virus type 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of a immunogenic stimulation factor especially a granulocyte-macrophage colony stimulation factor especially a granulocyte-macrophage the vaccines, which may be multivalent, are particularly used to protect dogs, cats and horses against bacterial and viral diseases, particularly those caused by the paramyxoviridae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 435 BP; 109 A; 132 C; 105 G; 89 T; 0 U; 0 Other;
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                                           Example 10; Fig 26; 109pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 435; Conservative
e.g. herpes virus
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This sequence represents the gene encoding a horse granulocyte-macrophage colony stimulating factor (GM-CSF). The gene was isolated from horse lymphocytes using a reverse transcriptase PCR method with primers ARF28954-AAF28950. GM-CSF induces colony formation in various types of blood cells and particularly induces cytotoxicity of macrophages; ciffinited and causes recruitment of blood cells and particularly induces cytotoxicity of macrophages; compositions for horse, e.g. for protection seems recruitment of protein itself, are useful as adjuvants in immunogenic or vaccinating compositions for horses, e.g. for protection against equine herpes, tetanus, Borrelia burgdorferi, rabies etc. Also as non-specific stimulators of the immune system. In a specific example, plasmid pJP097, containing the sequence for equine GM-CSF was used to transform CHO-K1 cells and the transformants grown for 18 He hours. The culture supernatant was then added to culture medium being used to grow porcine bone marrow cells. After 14 days, the mean number of colonies per culture box was 12-15, compared with none for cells grown in absence of GM-CSF. Equine GM-CSF allows a reduction in the amount of immunogenic/vaccinating component required, and may induce a response in enimals that would otherwise be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel DNA encoding equine granulocyte-macrophage colony-stimulating factor, useful as adjuvant for vaccines and as non-specific
inflammation; vector; adjuvant; immunogen; vaccination; vaccine; equine herpes; tetanus; Borrelia burgdokferi; rabies; gene; ds.
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                                                                                                                                                                                                                                                            "equine GM-CSF"
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andreoni CMP;
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P-PSDB; AAB37147.
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immunostimulant
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recombinant gamma-interferon, a cytokine-like molecule. The ovine cytokines will be useful in the intensive livestock industries such as live animal export trade, feed-lots and intensive rearing industries, where animals are subjected to great environmental challenge with infectious diseases, partic. respiratory infections, and are more prone to immunodepressive effects. The cytokines may be used for treatment or prophylaxis to maintain, stimulate or enhance immunoresponsiveness. They may also be useful as natural adjuvants for vaccines for sheep and cattle. See also AAQ24293-305, AAQ42311-15, AAQ24317-18 and AAQ25857-58. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Granulocyte-macrophage colony stimulating factor; GM-CSF; ds; gene, antibacterial; antiviral; vaccine; animal; immunogen; DMRIE; cationic lipid; quaternary ammonium salt; canine distemper virus; canine parainfluenza virus; canine herpes virus; feline herpes virus; equine herpes virus; dog; cat; horse.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                   Length 432;
                                                                                                                                                                                                                                                                                 Sequence 432 BP; 101 A; 138 C; 103 G; 90 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                 Query Match

83.5%; Score 363.2; DB 2
Best Local Similarity 90.0%; Pred. No. 1.8e-91;
Matches 389; Conservative 0; Mismatches 43
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27-JUN-2003
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                                                                                                                                      TACAAGCACTGCCCCCCCCCTGGAAACTTCCTGTGCAACCGATGATGATCACCCTC
                                                                                                                                                                                                             AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG
             TACAAGCAGCACTGCCCCCCCCCCCTGGAAACTTCCTGTGCAACCCAGATGATCACCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Granulocyte-macrophage colony-stimulating factor; immuno-depression; vaccine adjuvants; cytokine; ss.
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note= "putative signal sequence"
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'note= "GM-N PCR primer"
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/note= "GM-C PCR primer"
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/*tag= b
/note= "mature protein"
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/note= "ovine GM-CSF"
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27-OCT-1992
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allegies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAZ55575-Z5580 represent cDNA sequences encoding feline granulocyte macrophage colony-stimulating factor (GMCSF). The invention relates to canine interleukin-4 (IL-4), canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IRP-alpha) and feline GMCSF, and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including
Granulocyte macrophage colony-stimulating factor; GMCSF; antibody; feline; inhibitor; immune response; immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease.
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Pred. No. 7e-83;
0; Mismatches 64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Feline GMCSF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1k; Page 251-252; 264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                        AAZ55575 standard; cDNA; 444
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Best Local Similarity 85.3%;
Matches 371; Conservative (
                                                                          435
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                                                                                                                                                                                                                                                                                                                                                                               Feline GMCSF cDNA
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                                                                                                                                                                                                                                                                                                                                 14-MAR-2000
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                                                                                                                                                                                        AAZSSS75
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                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel DNA vaccine against pathogens that affect pets and sports animals comprises a plasmid containing a sequence, expressible in vivo, that encodes an immunogen from the relevant pathogen and a cationic lipid containing a quaternary ammonium salt, particularly N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium (DNRIE). The immunogens are particularly taken from canine distemper virus (CBV), canine parainfluenza virus type 2 (CPL-2), canine herpes virus type 1 (FHV-1), equine herpes virus type 1 (FHV-1), equine herpes virus type 1 (EHV-4). The method may also include the use of a immunogenic stimulation factor especially a granulocyte-macrophage colony stimulation factor especially a granulocyte-macrophage colony stimulation factor especially a granulocyte-macrophage colony stimulation factor especially a granulocyte-macrophage colony stimulation factor especially a granulocyte-macrophage colony stimulation factor especially a granulocyte accines, which may be multivalent, are particularly uses to protect dogs, cats and horses against bacterial and viral diseases, particularly the quaternary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ammonium salt provide a better immune response and thus more efficient protection, particularly when administered subcutancously. This sequence represents the gene encoding a feline GM-CSF used in the invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                    DNA vaccine containing plasmid and cationic lipid containing guaternary ammonium salt, useful for protecting pets and sports animals against, e.g. herpus virus.
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Pred. No. 7e-83;
0; Mismatches 64; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 435 BP; 116 A; 121 C; 102 G; 96 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                      Audonnet JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Fig 24; 109pp; French.
                                                                                                                                                                                                                                                                                      Fischer LJ, Barzu-Le Roux S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.5%;
                                                                                                                          08-JUN-2000; 2000WO-FR001592.
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99US-0144490P
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Best Local Similarity
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Sequences AAZ55575-Z5580 represent cDNA sequences encoding feline
granulocyte macrophage colony-stimulating factor (GMCSF). The invention
relates to canine interleukin-4 (IL-4), canine or feline Flt-3 ligand,
canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5,
canine IL-13, feline interferon-alpha (IRN-alpha) and feline GMCSF, and
nucleotides which encode these immunoregulatory proteins. The proteins,
their associated nucleic acids, specific antibodies and inhibitors may be
created as vaccines for therapeutic or prophylactic regulation of an immune
response in animals (particularly cats, dogs, horses and humans). They
may be used to treat autoimmune or infectious diseases including
allergies, tumours, inflammation and graft rejection, and to increase the
response from a co-administered antigen. The nucleotide sequences can
also be used for the recombinant production of a protein, while
calso be used for the recombinant production of a protein, while
cas sources of inhibitory threapeuties (e.g., antisense alignoucleotides).
The proteins may be used to raise antibodies and to screen for modulators
of activity, while the antibodies may be used in detection, and in drug
Claim 1k; Page 253; 264pp; English.
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                        Granulocyte macrophage colony-stimulating factor; GMCSF; antibody; feline; inhibitor; immune response; immunoregulation; tumour; cancer; autoimmune disease; vaccine; 8s.
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/product= "Feline GMCSF"
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complement(1. .435)
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Sequence 444 BP; 94 A; 104 C; 127 G; 119 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                64;
                                                                                                                                DB 3;
                                                                                                                         Query Match 76.5%; Score 332.6; DB Best Local Similarity 85.3%; Pred. No. 7e-83; Matches 371; Conservative 0; Mismatches 6
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XX AC AAQ6
XX AAQ OT 10-1
DI 10-1
DI 07-1
XX CYE
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The present invention relates to a method of optimising a coding sequence for expression of a protein, based on the amino acid sequence of the protein. This involves the use of a computer to generate a test sequence with m optimisation positions determined for a defined region, in which positions the codon usage is varied. The optimum codon usage at such positions is determined by means of a power function. The steps are relevanted with different regions of the sequence, with the optimised codons previously identified being left unchanged during subsequent steps. The method can be used for expression of proteins. The present sequence is the human GM-CSF wild-type coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAA 240
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390 AAAAGTTTCAAAGACAGTCTGAACAAATTTČTTTTACCATCCCCTTTGACTGCTGGGGG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer optimization of a nucleotide sequence for a protein comprises evaluating test sequences with a quality function to determine the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds; gene; human; GM-CSF; codon optimisation; protein production.
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Pred. No. 1.3e-82;
0; Mismatches 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GM-CSF wild-type coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 1; 83pp; German.
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                                                                                                                                                                                                                                                                                                                         ADQ76022 standard; DNA; 435 BP
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells, in xenogeneic transplantation. The cytokine may be used to prevent or treat various swine diseases, e.g. African swine fever, Hog cholera, Pseudorabies, etc. See also AAQ64863-80. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of a porcine cytokine gene designated chimerism enhancing fuctor (CHEF-2). The cytokine can be used for improving engrafment, stabilisation and proliferation of tissues, esp. bane marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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           kenogeneic cells; bone marrow; African swine fever; Hog cholera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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85.3%; Pred. No. 8.8e-83;
iive 0; Mismatches 64;
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                                                                                                                                                                                    ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monroy RL,
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/note= "signal"
100. .464
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Matches 371; Conservative
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                                                   Pseudorabies; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel process for modifying nucleic acid for a vectored expression modulation by targeted insertion or removal of CpG dinucleotides. The invention also describes modified nucleic acids and vector expressions. The process commences with the expression from tissue of a sample substance containing the target nucleic acid sequence, followed by its modification to increase or decrease the genetic expression of CpG di-nucleotides present, by degeneration of the genetic code. The modified target nucleic acid sequence is cloned with the operationally linked with a suitable transcription regulatory sequence. The modified target nucleic acid sequence is then expressed in a modified target nucleic acid sequence is then expressed in a modified for incorporation in a vectored expression in e.g. transgenic animals, medical therapy or vaccines. The process extends the usable range of
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                                                TACAAGCAGCACTGCCCCCCCCCTGGAAACTTCCTGTGCAACCCAGATGATCACCTTC 360
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                                                                                                                                                                                                                                                                                          gene; vector; expression; GM-CSF
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                     Human GM-CSF wild-type (10CpG) DNA.
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                                                                                                                                                                                                               0; Gaps
genetic expression. This sequence encodes human wild-type GM-CSF containing 10CpG, used in the process of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capsid protein; FCV strain 431; FCV strain G1; vaccine; cat; ds.
                                                                                                                    DB 15; Length 435;
                                                                                                               Query Match 76.2%; Score 331,6; DB 15; Length Best Local Similarity 85.3%; Pred. No. 1.3e-82; Matches 370; Conservative 0; Mismatches 64; Indels
                                                                     Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of GM-CSF gene clore 3R4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "GM-CSF"
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11-FEB-2000; 2000FR-00001761.
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                                                                                                                                                                                                            The present sequence encodes a cat GM-CSF protein. The specification describes the capsid proteins of feline calcivitus (FCV) strain 431 and strain G1. Cappsid proteins, derived from the FCV strains G1 and 431, induce antibodies that neutralize a wide variety of strains from different parts of the world. Vectors contening capsid encoding sequences are used as immunogenic compositions or vaccines for protection of cats against feline calcivirus, including use in multivalent vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding capsid protein of feline calcivirus, useful for producing vaccines that protect against many different strains of the virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            76.1%; Score 331.2; DB 4; Length 432; 85.4%; Pred. No. 1.7e-82; Live 0; Mismatches 63; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 432 BP; 115 A; 121 C; 101 G; 95 T; 0 U; 0 Other;
                                                                                                                                                                       Example 10; Fig 8; 62pp; French
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                      WPI; 2001-159521/16.
P-PSDB; AAB67464.
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Ното заріепв

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thuman pathogens and/or their components or human tumour calls and human pathogens and/or their components or human tumour calls and human peripheral blood lymphocytes. Also claimed is a vaccine comprising a cell codified to express an artigen and an immune-modulating protein, this is preferably an expression vector comprising a polynucleotide sequence that canceds the antigen and immune-modulating protein. Such vectors can be used to treat a subject having a tumour by transferring the expression vector into the tumour so that the antigen and the immune-modulator are expressed by at least the tumour. The methods can be used for producing and evaluating vaccines including cancer vaccines and vaccines directed against human pathogens, e.g. HIV, Leishmania, Mycobacterium, Listeria or Plasmodium. This sequence is an intermediate retroviral vector derived from pluMs, a vector approved for clinical use in the United States. pluL is essentially pluL6 digested with Call and Boll to remove cloning sites and the pluL6 internal Syneo gene. These were replaced with a polylinker.

CS Aneo gene was then inserted under the transcriptional control of the Sy40 enhancer/promoter to create the vector pluN. Two primers (AAV83185, AAV83186) were used to amplify the granulocyte macrophage colony

CS stimulating factor (GM-CSF) gene (AAV83189) for its insertion into pLSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunodeficient mice comprising human cells can be used for exposure to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of immunodeficient mice comprising human cells - particularly SCTD/beige mice comprising human immune cells for evaluating vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       against cancers or human pathogens, e.g. HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1b; Page 103-104; 154pp; English.
                                                                   97US-00838702.
97US-00848760.
97US-0069163P.
98WO-US006944.
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-024005/02
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Matches 370; Conserv
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The invention relates to a novel DNA vaccine against pathogens that affect pets and sports animals comprises a plasmid containing a sequence, expressible in vivo, that encodes an immunogen from the relevant pathogen and a cationic lipid containing a quaternary ammonium salt, particularly
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against,
                                                                                                                                                                                                                              361 GAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAG
                                                         181 TCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAG
                                                                                                                                                                 301 TACAAGCAGCACTGCCCTCCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTT
                                                                                                                                                                                                           361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG
                                                                                       Granulocyte-macrophage colony stimulating factor; GM-CSF; ds; gene; antibacterial; antiviral; vaccine; animal; immunogen; DMRIE; cationic lipplé; quaternary ammonium salt; canine distemper virus; canine parainfluenza virus; canine herpes virus; feline herpes virus; equine herpes virus; to horse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feline granulocyte-macrophage colony stimulating factor gene 3R3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA vaccine containing plasmid and cationic lipid containing ammonium salt, useful for protecting pets and sports animals e.g. herpes virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "feline GM-CSF 3R3
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                                                                                                                                                                                                                                                                                                                                                                              BP.
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                                                                                                                                                                                                                                                                     CCAGCCCAGAAGTAA 435
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/product=
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27-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                             the secretion of a heterologous protein from insect cells. The protein is expressed as a fusion protein, and is encoded by a polynucleotide comprising, in the 5' to 3' direction, a promoter, a signal peptide, an insect secretion competent polypeptide which is not an immunoglobulin For region and a heterologous protein with the coding sequences linked in frame. The expression cassette and vector are used for the production of heterologous peptides and proteins in insect and mammalian cell. The present sequence encodes a human granulocyte macrophage colony stimulating factor (GMCSF) (a secretion component). It is used to
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AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
               361 GAAAGTTTCAAAGAGAAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAG 420
                                                                                                                                                                                                                                                                                  Expression cassette; insect cell; insect secretion competent polypeptide; fusion protein; protein production; granulocyte macrophage colony stimulating factor; GMCSF; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification describes an expression cassette which is useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression cassette contains a promoter, signal peptide, secretion competent polypeptide and heterologous protein for production and secretion of heterologous peptides from eukaryotic cells.
                                                                                                                                                                                                                                                       DNA sequence of granulocyte macrophage colony stimulating factor
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85.1%;
                                                         CCAGCCCAGAAGTAA 435
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                                                                                                                                                               AAA64392 standard; DNA; 435
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/product= "GM-CSF"

WO2003031464-A2

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N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanamonium (DMRIE). The immunogens are particularly taken from canine Aietemney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide remodeling, glycoconjugation, glycosyltransferase, glycan;
granulocyte-macrophage colony stimulating factor; GM-CSF; human; gene;
ds.
                                                                                                                                                                                                                               AGTTCACCCAGCTCTGTCACTCGGCCCTGGCAACACGCGGAGGATGCCATCAAGGAGGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                   CGCCAACCCAGCCCTGTCACTCGGCCCTGGCATGTGGATGCCATCAAGGAGGCCCTG
                                                                                                                                                                                                                                                                                      TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAA
                                                                                                                                                                                  .
                                                                                                                                                76.1%; Score 331; DB 4; Length 435; 85.1%; Pred. No. 2e-82;
                                                                                                                               Sequence 435 BP; 117 A; 120 C; 101 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                 65; Indels
                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                 Matches 370; Conservative
                                                                                                                                                         Local Similarity
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2003-449162/42. P-PSDB; ABR55847

(NEOS-) NEOSE TECHNOLOGIES INC

28-AUG-2002;

2001US-0344692P. 2001US-0334233P. 2001US-0334301P. 2002US-0387292P 2002US-0391777P 2002US-0396594P 2002US-0404249P 2002US-0407527P

19-OCT-2001; 2 28-NOV-2001; 2 28-NOV-2001; 3

07-JUN-2002; 25-JUN-2002; L6-AUG-2002; 17-JUL-2002;

10-OCT-2001;

2002WO-US032263

09-OCT-2002;

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The invention relates to a cell-free, in vitro method of remodeling a peptide. The method involves removing a saccharyl subunit from the peptide. The method involves removing a saccharyl subunit from the peptide. The method involves removing a saccharyl subunit from the copy and with at least one glycosyl ransferase and at least one glycosyl donor under conditions suitable to transfer at least one glycosyl donor to the truncated glycan, thus remodeling the peptide. Conjugates can be formed between a granulocyte colony stimulating factor (G-CSS) peptide, interferon alpha peptide, interferon beta peptide, Factor VIIa peptide, conterferon gamma peptide, alpha-l-protease inhibitor (A-PI) peptide, interferon-gamma peptide, alpha-l-protease inhibitor (A-PI) peptide, interfleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha creceptor/immunoglobulin (Ig) of fusion peptide, urokinase peptide, anti-copportein IIb/III monoclonal antibody peptide, chimeric anti-HBR2 antibody peptide, anti-respiratory syncytial virus (RsV) F peptide, anti-copone antibody peptide, and a modifying group, where the modifying group is covalently attached to the peptide (HBSAG), human growth correspondent to the peptide (Hrough an interd glycosyl linking group. The method is useful for a cell-free, in vitro method of remodeling the above mentioned peptides. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remodeling a peptide, by removing a saccharyl subunit from the peptide to form truncated glycan, and adding or deleting glycosyl groups to a peptide and/or adding modifying group of a peptide to remodel the
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Location/Qualifiers

Homo sapiens.

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This invention relates to novel erythropoietin (EPO) peptides and the remodelling and glycoconjugation of these naturally occurring peptides thereof. Specifically, each EPO peptide comprises one or more glycans and has a glycoconjugate molecule such as polyethylene glycol (PEG) attached to it. Accordingly, the present invention provides glycoPEGylated EPO peptides that have either monoantennary, biantennary or triantennary glycans covalently attached thereto. As such, these peptides are useful for the treatment of anaemia, and hence exhibit antianaemic activities working to increase haematocrit levels in mammals, in particular in
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glycoPEGylated BPO peptide; anaemia; antianaemic; haematocrit level;
kidney dialysis; haematology;
granulocyte-macrophage colony stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human granulocyte-macrophage colony stimulating factor DNA SeqID 17.
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06-JAN-2003; 2003US-00360770.
19-FEB-2003; 2003US-00360779.
09-APR-2003; 2003US-00410945.
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P-PSDB; ADN49690.
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humans i.e. increasing the relative volume of blood occupied by erythrocytes. Furthermore, EPO therapy can be used to treat kidney dialysis patients. This polynucleotide is a human DNA sequence related the field of haematology, given in an exemplification of the invention.
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TYPE: DNA
CORGANISM: Homo sapiens
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                                                                                                               May 26, 2006, 01:26:24; Search time 132 Seconds (without alignments) 372.005 Million cell updates/sec
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EMC Celerra SIDS3/ptodata/2/pubpna/US09 NEW PUB.seq:*

FEMC Celerra SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

FEMC Celerra SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

EMC Celerra SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

EMC Celerra SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

EMC Celerra SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

EMC Celerra SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

EMC Celerra SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

EMC Celerra SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Sequence 1765,
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US-09-484-331-27

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US-09-484-331-27

US-09-484-331-8

US-09-484-331-8

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US-09-484-331-8

US-10-946-650-49

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## ALIGNMENTS

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US-11-183-118-17

Sequence 17, Application US/11183218

Publication No. US2006008906A1

GENERAL INFORMATION:
APPLICANT: Defences, Shawn
APPLICANT: Deferees, Shawn
APPLICANT: Deferees, Shawn
APPLICANT: Deferees, Shawn
APPLICANT: Deve, Caryne
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryne
TILE REFERENCE: 040683-01-5083-0202
TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF BRYTHROPOIETIN
FILLING DATE: 2005-07-15
PRIOR FILLING DATE: 2005-07-15
PRIOR FILLING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PLILING DATE: 2002-08-28
PRIOR FILLING DATE: 2002-09-16
PRIOR FILLING DATE: 2002-09-16
PRIOR FILLING DATE: 2002-09-16
PRIOR FILLING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US 60/394,692
PRIOR FILLING DATE: 2002-06-25
PRIOR PLILING DATE: 2001-11-19
PRIOR PLILING DATE: 2001-11-28
PRIOR FILLING DATE: 2001-11-28
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Pred. No. 2.8e-85;
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SEQ ID NO 17
LENGTH: 435
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APPLICANT: Woldgemuth, Jay
APPLICANT: Woldgemuth, Jay
APPLICANT: Woldgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Perentice, James
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REPERENCE: S06612000104
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR PILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-01-220
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.1%; Score 331; DB 6; Length 781; Best Local Similarity 85.1%; Pred. No. 3.5e-85; Matches 370; Conservative 0; Mismatches 65; Indels
 Indels
 65;
 0; Mismatches
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 Matches 370; Conservative
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US-10-511-937-396
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LENGTH: 781
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33 ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCC 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 GAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAG
                                                                                                                                                                              361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG
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GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Perentice, James
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: MUMBER: US/10/511,937
CURRENT APPLICATION NUMBER: PA101
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-10-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 64
TANGTH: GO
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Pred. No. 0.009;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/10511937; Publication No. US20060088836A1; GENERAL INFORMATION:
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Best Local Similarity 86.03
Matches 43; Conservative
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RESULT

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1362 GGCCCCATCAGCCACCAGGGGCAGCAGCTGATGACGCTGCAGCGCCACGTGCAGGGCTGT 1303
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                                   196 GCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAAAACAGGGCTTGCGGGGC 255
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Pred. No. 1.1;
0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1196, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION: US20060105376A1
GENERAL INFORMATION: US20060105376A1
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 2243
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GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1692
LENGTH. 2562
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7.8%; Score 33.8; Di
Best Local Similarity 53.4%; Pred. No. 1.1;
Matches 71; Conservative 0; Mismatches
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Best Local Similarity 53.4%;
Matches 71; Conservative (
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CORGANISM: Homo sapiens
US-11-293-697-1196
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ORGANISM: Homo sapiens
US-11-293-697-1692
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                   Sequence 113, Application US/10468193

Publication No. US20060100416A1

Publication No. US20060100416A1

GENERAL INFORMATION:
APPLICANT: Palli, Subba R.
APPLICANT: Cress, Dean E.
APPLICANT: Monan B.
TITLE OF INVENTION: Receptor-Based inducible Gene Expression System
FILE OF INVENTION: Receptor-Based inducible Gene Expression System
FILE REFERENCE: A01247-US
CURRENT APPLICATION NUMBER: US/10/468,193
CURRENT APPLICATION NUMBER: US 60/313,925
FRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 113
SOSTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 769 CTGCCATCGTGTACGACTCTCGCGTGTACGGCTGGTTGTTGGCGAACAGGATCGAGTCTG 710
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TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION WUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
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Publication No. US20060105376A1
GENERAL INFORMATION:
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; ORGANISM: Nephotetix cincticeps
US-10-468-193-113
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Conservative
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; ORGANISM: Homo sapiens
US-11-293-697-965
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Best Local Similarity
Matches 71; Conserv
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US-10-468-193-113/c
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LENGTH: 1109
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1167 AGCTGTGGGAGCTGCTCAAGAAGGACAACACCTACGTCTACATGTGCGGGCTCAAGGGCA 1226
1107 AGACGAACGCGGCCGGGGAGAAGATGTACATCCAGACGCGCATGGCGGAGTACAAGGAGG 1166
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Publication No. US20060105318A1
GENERAL INFORMATION:
APPLICANT: HARRITON:
APPLICANT: SHERP, BRUCE
APPLICANT: RUNDLETT, STEPHEN
TITLE OF INVENTION: COMPOSITIONS GENES
FILE REFERENCE: 0221-0003L
CURRENT APPLICATION UNMBER: US/09/484,331
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: 09/276,820
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48.2%; Pred. No. 3.1;
tive 0; Mismatches 99; Indels 0.
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APPLICANT: Borrelly, Gilles
APPLICANT: Borrelly, Gilles
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Drittante
TITLE OF INVENTION: MODIFIED GROWTH HORMONES
FILE REFERENCE: 17109-015001/925
CURRENT APPLICATION NUMBER: US/11/267,871
CURRENT FILING DATE: 2005-01-03
PRIOR FILING DATE: 2005-08-08
PRIOR FILING DATE: 2005-08-08
PRIOR FILING DATE: 2005-08-08
NUMBER OF SEQ ID NOS: 719
SOFTWARE: PastSEQ for Windows Version 4.0
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Publication No. US20060094655A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 92, Conservative
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US-11-267-871-717
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US-10-953-349-35010
US-10-953-349-35010
Sequence 35010, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: UNMBER: US/10/953,349
CURRENT APPLICATION UNMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 35010
LENGTH: 1628
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1846 GCCGGGGAGGCCCGAGGCCTGTAGCCTGGACAGCTGCAAGGGCCCTGGGTCCCCCCC 1787
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Publication No. US20060105376A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SEQ ID NO 1541
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Pred. No. 1.2;
0; Mismatches
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CORGANISM: Homo sapiens
US-11-293-697-1541
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Best Local Similarity
Matches 70; Conserv
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US-11-293-697-1541/c
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Publication No. US20060105318A1

Publication No. US20060105318A1

GENERAL INPORMATION:
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHERF, BRUCE

APPLICANT: RUNDLETT, STEPHEN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF TITLE OF INVENTION: ENDOGRNOUS GENES
FILE REFERENCE: 0221-0003L

CURRENT APPLICATION NUMBER: US/09/484,331

CURRENT APPLICATION NUMBER: 09/276,820

PRIOR FILING DATE: 1999-03-26
                                                               2262 AGAAAAGGGGCCATTTTCCACCATGATATTGGGCAAGGCATGGCATGGGTCACGAC 2321
                                                                                                                     199 GAGGAGCTGACTGCAGACTCGCCTGAAGCTGTACAAACAGGGCTTGCGGGGCAGC 258
                                                                                                                                                                                                                                259 CTCATCAAGCTCGAAGGCCCCTTGACCATGATGGCCAGCACTACAAGCAGCACTGCCCC 318
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US-10-485-397-10/c
; Sequence 10, Application US/10485397
; Publication No. US2006099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTAMA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B697USCT01
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.5%; Score 32.6; DB 6; Length 5264; Best Local Similarity 48.2%; Pred. No. 3.2; Matches 92; Conservative 0; Mismatches 99; Indels 0
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; OTHER INFORMATION: pSEAPstopneo is a circular Plasmid DNA
US-10-485-397-10
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US-09-484-331-27
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APPLICANT: SHERF, BRUCE
APPLICANT: SHERF, BRUCE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION: ENDOGENOUS GENES
FILE REPERENCE: 2021-00031
CURRENT APPLICATION NUMBER: 09/276,820
PRIOR FILING DATE: 1999-03-06
PRIOR FILING DATE: 1999-03-06
PRIOR FILING DATE: 1999-03-06
PRIOR FILING DATE: 1999-02-19
PRIOR FILING DATE: 1999-02-19
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PRIOR FILING DATE: 1999-02-19
PRIOR FILING DATE: 1999-02-19
PRIOR FILING DATE: 1999-02-16
SPIOR PLICATION NUMBER: 09/159,643
PRIOR FILING DATE: 1999-03-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 20
LENGTH > 5.47
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PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 09/263,814
PRIOR PILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/253,022
PRIOR FILING DATE: 1999-02-19
PRIOR FILING DATE: 1999-02-19
PRIOR PILING DATE: 1998-09-24
PRIOR PILING DATE: 1998-09-24
PRIOR PILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTER OF SEQ ID NOS: 33
SOFTWARE: PATENTER OF SEQ ID NOS: 33
LENGTH: 4644
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CORGANISM: Homo sapiens
US-09-484-331-19
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US-09-484-331-20
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US-09-484-331-20
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Publication No. US20060099673A1

GENERAL INFORMATION:
TILLE OF INVENTION: Novel Recombinant Gene Expression Method
FILE REPERENCE: B697USPCT01

CURRENT APPLICATION NUMBER: US/10/485,397

CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Pitentin version 3.0

LENGTH: 5408

TYPE: DNA

ORGANISM: Artificial

PEATURE:
PRATURE:
PATURE:
COTHER INFORMATION: pSEAPStopMneo is a circular Plasmid DNA
US-10-485-397-9
                                                                                                                                                                                                                                                                                                                                                     7.5%; Score 32.6; DB 1; Length 5314;
48.2%; Pred. No. 3.3;
tive 0; Mismatches 99; Indels 0;
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PRIOR APPLICATION NUMBER: 09/263,814
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-02-19
PRIOR FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: 09/159,643
PRIOR APPLICATION NUMBER: 08/941,223
PRIOR FILING DATE: 1991-09-26
NUMBER OF SIQ ID NOS: 33
SOFTWARE: PATCENTIN VET: 2.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.23
Matches 92; Conservative
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US-09-484-331-27
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Db 2704 TGTCGCTCGA 2694

Search completed: May 26, 2006, 01:31:24
Job time: 133 secs
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DO053415 Homo sapi
AW207707 UI-H-BI2-
BEZ18982 hv47a07.x
AI912784 we13607.x
BEG71554 7653h07.x
BEG69962 7627908.x
DO053416 Pan trog1
CF341802 TGEST2YJ4
BER73976 601484045
CF370966 TGEST2YJ5
CF370966 TGEST2YJ5
BX111836 BX111836
CR457551 714908 MA
BM539160 hb05e10.9
CFG14774 CES009199
BF938995 7703f11.x
CB430266 606148 MA
CV700569 TGEST2YSS
                                                                            (without alignments)
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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BX111836
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RESULT 1						
DQ053415 LOCHS	2	053415			435 bp DNA linear	GSS 02-JUN-2008
DEFINITION		Homo sapiens	C 3	003	ne,	al seq
		genomic survey		sednence		
ACCESSION VERSION		DQ053415 DQ053415.1	GI:66	:668993	862	
KEYWORDS	SS				•	
SOURCE			ns (human)	an)		
ORGANISM		Homo sapiens	ns		110000	
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		Hominidae;	#			
REFERENCE		l (bases l Nielsen P	1 to 435) Bustama	5) mant	מ אוייים[ח	A T Corton
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TITLE	A i	Scan for Posi	Positi	vel)	ted denes i	of Humans and
TAMOTOL		Chimpanzee (er) bios	g Fiol	(9)	E170 (2005)	
PUBMED	·	325	;	)		
REFERENCE		(bases	1 to 43	435)		
AUTHORS		Nielsen, R.	, Busta	mant	G., Gla	Sackton, T.B.,
	3 3	DISZ,M.O	, Fledel-A	- 1 - 1	., lanenbaum Adams M D a	
TITLE	Di	Direct Submission	nission			
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1. .435 /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606"

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Email: cgapbs-r@mail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2724184"
/lab host="DH108 (Life Technologies)"
/clone lib="NCT_CGAP_Sub4"
/note="Vector: pT7130-Pac1; Site 1: Not I; Site 2: Eco RI;
The NCI_CGAP_Sub4 library is a subtracted library derived
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1 (bases 1 to 588)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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1456009-1456775, 1500552-1502855) NCI CGAP Kid5 pool 1:
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDS
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDS
132391-3336-3342, 3722-3725, 3776-3778 (IMAGE CloneIDS
132391-1325831, 1471368-1472903, 1492104-1493255)
NCI CGAP LuS pool 1: LLAM 3575-3582, 3851-3864 (IMAGE
CloneIDS 1414920-1417991, 1520904-1522439) NCI CGAP GC4
pool 1: LLAM 3164-1167, 3716-3720, 3733-3735 [IMAGE
CloneIDS 1257096-1258631, 1469064-1470983,
1475592-1476743) NCI CGAP PC2 pool 1: LLAM 2457-2459,
2758-2759, 3062-3068 (IMAGE CloneIDS 98508-986759,
1101192-1101959, 1217928-1220615) NCI CGAP Col0 pool 1:
LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 1057416-11061255,
1144584-114531) Subtraction was performed as previously described [Bonnaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Pacilitate Gene
TAG_INSUB-COlon
TAG_LIB=NCI CGAP_CO4
TAG_SEQ=CTTGGRAP
from the NCI CGAP Sub2 library which is a subtracted library derived from the NCI CGAP Sub1 library, which is a subtracted library derived from Blb Bl constitutes a mixture of 21 normalized or subtracted NCI CGAP [1] braries: NCI CGAP CO4, NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP CO10, NCI CGAP CO16, NCI CGAP Kid1, NCI CGAP Library, NCI CGAP Exid CGAP Rid CGAP CO10, NCI CGAP Library, NCI C
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85.1%; Pred. No. 6.2e-83;
iive 0; Mismatches 65.
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Best Local Similarity 85.1
Matches 370; Conservative
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424

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/unclear INAGE: 1340997"

/tissue type="carcinoid"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="Dh10B"
/lab_host="Dr2d"
/lab_host="lab_not_" CGAP_Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac1; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and sscircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCF amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento
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Insert Length: 743 Std Error: 0.00
Beg primer: -40UP from Gibco
High quality sequence stop: 447:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1912784 666 bp mRNA linear EST 18-DEC-1999 well3f0'.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:2240997 3' similar to gb:M11220 GRAUULOCYTE-MACROPHAGE COLONY-STIMULATING PACTOR PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                             361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
                                                       TACAAGCAGCACTGCCCCCCCCCCCCGGAAACTTCCTGTGCAACCCCAGATGATCACCTTC 360
                                                                                                                                     305 TACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCCAGATTATCACCTTT 364
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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1 (bases 1 to 666)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                  365 GAAAGTTTCAAAGAAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAG
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85.1%; Pred. No. 6.5e-83;
ive 0; Mismatches 65
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL, send email to:
infoatmage.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stopp: 445.
                                                                                       BE218982

bv47a07.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3176532 3'
similar to gb:M11220 GRAMUJOCYTE-MACNOPHAGE COLONY-STIMULATING
FACTOR PRECURSOR (HUMAN); mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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/lab_host="DH108"
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/db_xref="taxon:9606"
/clone="IMAGE:3176532"
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                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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695 bp mRNA linear EST 08-SEP-2000 7e2/g08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3283742 3' similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN);, mRNA bequence. BE669962.1 GI:10030503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.lln.gov
reaction. The driver wab PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Patima Bonaldo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 695)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Email: Gagpbs-rømail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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Pred. No. 6.5e-83;
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                                                                                                                             76.1%;
85.1%;
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Email: gapbs-r@mail.nih.gov
Tinsue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tinsue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@immer: -40UP from Gibco
Seq primer: -40UP from Gibco
High quality sequence stop: 440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7e53h07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3286237 3' similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING PEACTOR PRECURSOR (HUMAN);, mRNA sequence.
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//clone lib="NCT_CGAP_Lu24"
//note="Organ: lung; Vector: pT773D-PacI; Plasmid DNA from
//note="Organ: lung; Vector: pT773D-PacI; Plasmid bNA from
//close nere made in vitro_Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                            CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGGTGTGGATGCCATCAAGGAGGCCCTG
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I (bases 1 to 672)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3286237"
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/lab_host="DH10B"
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TGEST291431602.V1 TG CAST Tachyzoite cDNA Library TOXOplasma gondii cDNA clone TGEST275/3431602.V1 S similar to SW.CSF2 HUMAN P04141
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR FRECURSOR; MRNA
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                                                                                 (bases 1 to 435)
(bases 1 to 435)
(bases 1 to 435)
(bases 1, Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Pledel. Alon, A., Tadenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Burect Submission
Submitted (05-WAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                   of Humans and
                                                                                                                                                                                                     This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGIGGCIGCAGAGCCTGCTGCTCTTGGGCACTGTGGGCCTGCAGCATCTCTGCACCCGCC
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84.8%; Pred. No. 1.6e-82;
iive 0; Mismatches 66
White, T.J., Sninsky, J.J., Adams, M.D. A Scan for Positively Selected Genes Chimpanzees
                                                                                                                                                                                                                                                                 1. .435 / creatism="Pan troglodytes" / mol type="genomic DNA" / db xref="taxon:9598"
                                                   PLoS Biol. 3 (6), E170 (2005)
                                                                                                                                                                                                                                                                                                                                                             /locus_tag="HC14003"
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Best Local Similarity 84.8
Matches 369; Conservative
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Toxoplasma gondii
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                                                                                                                                                   /clone lib="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT773D-PacI; Plasmid DNA from Inte-"Organ: lung; Vector: pT773D-PacI; Plasmid DNA from the normalized library NCI CGAP Lu3 was prepared, and sscircles were made in vitro. Following HAP purfication, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435 bp DNA linear GSS 02-JUN-2005
Pan troglodytes HC14003 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Pan.
I (bases 1 to 435)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                 9
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Pan troglodytes
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 CGCTCGCCCAGCCCCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 TACAAGCAGCACCCCCCCCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCAACCCAGCCCTGTCACTCGGCCCTGGCATGTGGATGCCATCAAGGAGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 TACAAGCACTGCCCCCCCCCCCGGAAACTTCCTGTGCAACCCAGATGATCACCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                             Score 331; DB 7; Length 695;
Pred. No. 6.6e-83;
0; Mismatches 65; Indels
                                                                                                                   /tissue_type="carcinoid"
/lab_host="DH108"
                                                     organism="Homo sapiens"
   ity sequence stop: 456.
Location/Qualifiers
                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3283742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQ053416
DQ053416.1 GI:66899363
GSS.
                                                                                                                                                                                                                                                                                                                                             76.1%;
85.1%;
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Best Local Similarity ...
...hes 370; Conservative
     quality
     High
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                                        source
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DQ053416
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EST 20-OCT-2000

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TACAAGCAGCACTGCCCCCCCCCCTGGAAACTTCCTGTGCAACCCAGATGATCACCTTC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 crcecccadececcadedecedecerdedadecarierdaaridecarecadeadecedede 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gacdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://imaga.llnl.gov
Plate: LLAM9663 row: j column: 12
High quality sequence stop: 711.
Location/Qualifiers
1. .895
                                                                                                           361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae, Homo.

1 (bases 1 to 895)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 Gregoriccacaaaccrecrircricgecacregerriracaecareceecacecee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE871976 895 bp mRNA linear EST 20-OC
601484045F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 895;
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85.0%; Pred. No. 2.6e-82;
ive 0; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE873976.1 GI:10322752
                                                                                                                                                                                                                                                                                       421 CCAGCCCAGAAGTAA 435
                                                                                                                                                                                                                                                                                                                                        453 CCAGTCCAGGAGTGA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="rggetary)aid.
/clone="rggetary)aid.
/dev stage="Tachyzoite"
/lab_host="ElectroTen Blue cells (Stratagene)"
/done lib="Tg CAST Tachyzoite cDNA Library"
/clone lib="Tg CAST Tachyzoite cDNA was sometracted by
Keliang rang, and Robert COle at Washington University.
CONA was synthesized from poly(A)+ mRNA using the
template-switching PCR method (SMART CDNA Kit, BD
Biosciences). First strand cDNA was reverse trand
synthesis was PCR amplified using the same primer set and
the fragments were digested with Sfil. The fragments were
size selected, ligated into a modified pBluescript vector
(obtained from Michael White, Montana State University)
containing directional Sfil sites, and electroporated into
ElectroTen Blue cells. Vector: Sfil sites were added to
the multiple cloning region of BBluescript SK between the
BanHI/ECORI sites. The modified polylinker has the
BanHI/ECORI sites. The modified polylinker has the
BanHI/ECORI sites. The modified polylinker has the
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                                                                                                                                                                                                                                                                                                                                                                                                              Email: toxo@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCCGCCTCGGCCCACGGATCC3'where n=3.4 G nucleotides. WARNING: the library contains a small percentage of CDNAs derived from the human host cells. Library materials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCAACCCAGCCCTGTCACTCGGCCCTGGCATGTGGATGCCATCAAGGAGGCCCTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                   Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hilier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   provided by David Sibley, Washington University."
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     Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
                                Sarcocystidae; Toxoplasma.
1 (bases 1 to 584)
                                                                                                                                                                                                                                  Unpublished (2001)
Contact: Clifton, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 04.0
Matches 369; Conservative
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the fragments were digasted with Sfil. The fragments were size selected, ligated into a modified pBluescript vector (obtained from Michael White, Wontana State University) containing directional Sfil sites, and electroporated into ElectroTen Blue cells. Vector: Sfil sites were added to the multiple cloning region of pBluescript SK+ between the Bamil/EcoRI sites. The modified polylinker has the following sequence: 5'GAATTGGCCATTAGGGC (G)n-. insert-GGCGCTGGGCCACGGATCG3' where n=3-4 G nucleotides. WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF370966 592 bp mRNA linear EST 27-AUG-2003
GPSGT24758612.y1 TG CAST TAChyzoite cDNA Library TOXOplasma gondii
cDNA clone TGSGT2y158612.y1 5 similar to SW:CSF2 HUMAN P04141
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR FRECURSOR ; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCAACCCAGCCCTGTCACTCGGCCCTGGCATGTGGATGCCATCAAGGAGGCCCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACAAGCAGCACTGCCCCCCCCCCCTGGAAACTTCCTGTGCAACCCAGATGATCACCTTC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sarcocystidae; Toxoplasma.

I (bases 1 to 592)
Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,
Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
Kitter,E., Bennett,J., Franklin,C., Tasgareishvili,R., Ronko,I.,
Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 CGCTCGCCCAGCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 GAAAGTTTCAAAGAGAACTGAAGGACTTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                       35 ATGTGGCTGCAGAGCCTGCTGCTTTGGGCATCTGTGGCCTGCACCTGTTCTGCACCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxoplasma gondii
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                                                               Length 585;
                                                                                                                                                                                                                                                                                                                                                                       70; Indels
                                                                                                                                                                                                                                                                                                                            74.3%; Score 323; DB 5;
83.9%; Pred. No. 1.2e-80;
ive 0; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF370966.1 GI:34318212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 CCAGCCCAGAAGTAA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccaerccaegaerea 469
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Constroe Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                    Similarity
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CF370966
LOCUS
DEFINITION
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/mol_type="mRNA"
/mol_type="mRNA"
/dow_tref="maxon:5811"
/clone="TgEGTzyj55612.yl"
/dev_stage="Tachyzoite"
/dab_host="ElectroTen Blue cells (Stratagene)"
/clone_lib="Tg CAST Tachyzoite cDNA Library"
/clone_lib="Tg CAST Tachyzoite cDNA Library"
/clone_lib="Tg CAST Tachyzoite cDNA Library"
/note="Vector: Modified pBluescript (pBS SK+); Site_1:
BamH1; Site_2: ECOR1; The CDNA library was constructed by
Kaliang Tang, and Robert Cole at washington University.
CDNA was synthesized from poly(A)+ mRNA using the
template-switching PCR method (SWART CDNA Kit, BD
Biosciences): First strand cDNA was reverse transcribed
using the CDS III/3' primer and a 5' template switch
primer (Smart IV primer). The product of the first strand
synthesis was PCR amplified using the same primer set and
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TGESTZYJ55e12.yl TG CAST Tachyzoite cDNA Library Toxoplasma gondii cDNA clone TGESTZYJ55e12.yl 5' similar to SW:CSF2 HUMAN P04141
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
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clone availability.
       Toxoplasma gondii
Toxoplasma gondii
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Eukaryota; Alveolata; Toxoplasma.

1 (bases 1 to 588)
Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M.,
Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,
Hillier, L., Buennett, J., Franklin, C., Tasgareishvili, R., Ronko, I.,
Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.,
Toxoplasma EST Project
                                                                       CAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGA
                                                                                                                                                                                                                                                                                                                                                    CAAGCACACCCCCCCCCCCCCCTGGAACTTCCTGTGCAACCCCAGATGATCACCTTCAA
                                                                                                                                                                                                                                                                                                                            AAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAGCC
                                                    TGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCA
                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: toxo@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu)
information relating to organism, libraries, or
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: Clifton, S.
                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCCAGAAGTAA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                    || |||| ||| || || || || AGTCCAGGAGTGA 433
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LOCUS
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VERSION
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SOURCE
ORGANISM
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JOURNAL
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AUTHORS
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EST 27-AUG-2003

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 658)
S Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Human Unigenese - RZPD3
L Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAG998(104661.
RZPD; IMAG98(104661.
RZPDI: M.A.G.E. cDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDIE No.972)
Human Unigeneset - RZPD3 (RZPDIE No.972)
Human Unigeneset - RZPD3 (RZPDIE No.972)
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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/tissue_type="carcinoid"
/tissue_type="carcinoid"
/tissue_type="carcinoid"
/lab_host="DH108"
/clone lib="NG1 CAAP Lubs"
/note="Organ: lung; Vector: pT773D-PacI; lst strand cDNA was prepared from neuroendoocrine lung carcinoid, and was then primed with a Not I - 01490(dT) primer.

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                           EST 07-FEB-2003
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                                                                                                                                                                                                                                                                                                                           BX111836
BX111836 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGp998C104061;
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larity 84.6%; Pred. No. 1.7e-79;
Conservative 0; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE:1601601, mRNA sequence.
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                                   421 CCAGCCCAGAAGTAA 435
                                                                                       455 CCAGTCCAGGAGTGA 469
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BX111836/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="mrkna"
//mol type="mrkna"
//mol type="mrkna"
//do xref="taxon:5811"
//clone="TgESTxyj58e12.y1"
//dows taage="Tachyzoite"
//lab host="ElectroTen Blue cells (Stratagene)"
//clone="TgESTxyj58e12.y1"
//dows taage="Tachyzoite"
//lab host="ElectroTen Blue cells (Stratagene)"
//clone="TgESTxyj58e12.y1"
//note="Vector: Modified pBluescript (DBS SK+); Site_1:
BamHi; Site_2: EcoRi; The cDNA library was constructed by
Kellang Tang, and Robert Cole at Washington University.
CDNA was synthesized from poly(A) + mRNA using the
template-switching PCR method (SMART CDNA Kit, BD
Bloscinces): First strand cDNA was reverse transcribed
using the CDS III/3' primer and a 5' template switch
primer (Smart IV primer): The product of the first strand
synthesis was PCR amplified using the same primer set and
the fragments were digested with Sfil. The fragments were
size selected, ligated into a modified pBluescript vector
(obtained from Michael White, Montana State University)
containing directional Sfil sites, and electroporated into
ElectroTen Blue cells. Vector: Sfil sites were added to
the multiple cloning region of pBluescript SK between the
BamHifcook sites: The modified polylinker has the
following sequence: 5'GAATTCGGCCATTACGGCC(G)n-. insert-
GGCCGCTCGGCCACGAGTCCA', where mail percentage of CDNAs
derived from the human host cells. Library materials
                                                                                                                                                                                                                                        Email: toxo@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seg primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 GAAAGTITCAAAGAGAACCTGAAGGACTITCTGCTTGTCATCCCCTTTGACTGCTGGAG 454
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                          Toxoglasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1810
Fax: 314 286 1810
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Pred. No. 1.2e-80;
0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .592
/organism="Toxoplasma gondii"
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity 83.9%;
Matches 365; Conservative (
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Seg primer: -2IM13UnivRev
High quality sequence stop: 572.
Location/Qualifiers
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Canis familiaris
                                                                                                                                                                                                                                                                                                                                                       421 CCAGCCCAGAAGTAA 435
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1 (bases 1 to 561)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J. B. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
pross_match v0.990329.
Plate: FQY8072 row: H column: 12
Seq primer: GTAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                      EST 26-MAR-2003
                                                          419
                                                                                     312
                                                                                                     372
                                                                                                                                                             373 AAGAACCIGAAGGAITITICIGITITGAGAICCCGTITGACTGCTGGAAGCCAGCCCAGAAG 432
                                                                                                                                                                                                                                    239
CTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAATGTTT 479
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                                            GACCTCCAGGAGCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGAGCAGGGCCTGCGG
                                                                                                                                            TGCCCCCCCCCCGGAAACTTCCTGTGCAACCCAGATGATCACCTTCAAAAGTTTCAAA
                                                                                                                                                                                                                        298 GAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /notes "Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including liver; lung, hypothalamus, pituitary, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                     CB457551 561 bp mRNA linear 714908 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .561
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC_6BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (cattle)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
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Best Local Simi
Matches 369;
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DEFINITION
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hboselo.gl Canis cDNAs from testes cells Canis familiaris cDNA clone hboselo 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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                  136
                                                                                                                                                                                                                                   TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAAGCTGTACAAA 240
                                                                                           194 TCTGAAAAGTTTGACTCCCAGGAACCAACGTGCCTGCAGACTCGCCTGAAAGCTGTACAAG 253
                                                                                                                                                                                                                                                                                                                                                                       254 AACGGCCTGCAGGGCAGCCTCACTAGTCTCATGGGCTCCTTGACCATGATGGCCACCAC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 TACGAGAAACACTGCCCACCCCACCCCGGAACTTCCTGTGGAACCCCAGTTTATCAGCTTC 373
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Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Hazor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 347 884
Fax: 516 347 884
CGCCCACCCAACACTGCCACCCGGCCCTGGCATGTGGATGTGGATGCCATCAAGGAGGCCCTG
                                                                                                                                               AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG
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/db_xref="taxon:9615"
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SIRVO Livestock Industries
Level 5, Queensland Bioscience Precinct, University of Queensland,
306 Carmody Read St. Lucia QLD Australia
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Mammalla; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos
1 (bases 1 to 672)
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CCL009198 5', mRNA sequence.
                                                            Gaps
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0
                                  Length 572;
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                                   DB 2;
any library related inquiries."
                                  Score 318.2; DB 2
Pred. No. 2.8e-79;
                                                          0; Mismatches
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Mamm. Genome 16 (3), 201-210 (2005)
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/mol_type="mRNA"
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Fax: 07 3214 2480
Email: Sigrid.Lehnert@csiro.au
Plate: 08 row: D column: 01.
Location/Qualifiers
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                                  73.1%;
83.2%;
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                                                Best Local Similarity 83.2
Matches 362; Conservative
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SOURCE
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/tissue_type="Longissimus dorsi muscle"
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/lab host="XIJ-BlueWRF' strain"
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EcoRI; Site_2: Xho I; Library made from skeletal muscle of a 14 month old Angus steer."
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84.1%; Pred. No. 2.1e-78;
ive 0; Mismatches 66;
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ne : 3398 secs
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Matches 366; Conservative
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US-09-589-460-8
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Matches 435,
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Sequence 111, App
Sequence 111, App
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/ EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*
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                                                                            May 26, 2006, 01:01:29 ; Search time 164 Seconds
GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-322-409-119
US-09-451-527-119
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Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 ; Gapext 1.0
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123	Sequence 3, Appli Sequence 7, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 275, Appli Sequence 275, Appli Sequence 175, Appli Sequence 10, 5391485 Patent No. 5391485 Patent No. 5391486
US-10-262-439-123 US-09-555-165-8 US-09-555-165-10 US-08-188-009-191 US-08-460-736-191 US-09-64-667-191 US-09-65-667-191 US-09-65-667-191 US-09-616-434-1195	NG-09-310-842-3 US-08-130-128-7 US-10-188-056-34 US-08-750-128-4 US-08-259-696B-8 US-08-259-696B-8 US-08-902-513-6 US-08-902-513-8 US-09-976-594-275 US-09-976-594-275 US-239496-1
10322 10322 44332 44355 44966 74966 7565 7565	1318 9445 9435 8069 8069 1011 6660 1588
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                                                                                                                                                                                                                                                                                                                        Length 435;
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100.0%; Pred. No. 5.2e-118;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                   ORGANISM: Equine sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(432)
OTHER INFORMATION: coding sequence of equine GM-CSF gene
Sequence 8, Application US/09589460
Patent No. 645740
GENERAL INFORMATION:
TITLE OF INVENTION: Equine GM-CSF
FILE REPERENCE: 454313-2334 1
CURRENT APPLICATION NUMBER: US/09/589,460
CURRENT FILING DATE: 1090-06-07
PRIOR PILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8: SEQ ID NOS: 9
LENGTH: 435
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APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ALD MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT PELLING DATE: 1999-05-28
EARLIER PAPLICATION NUMBER: 60/087,306
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1999-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                             ; Sequence 121, Application US/09322409; Patent No. 6471957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 119, Application US/09451527; Patent No. 6482403; GENEAL INFORMATION: APPLICANT: Sim, Gek-Kee
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Matches 371; Conservative
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US-09-451-527-119
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APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Wards, Shumhan
APPLICANT: Worderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
TILLE REPERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT APPLICATION NUMBER: 60/087,306
EARLIER PELING DATE: 1999-05-29
NUMBER OF SEQ ID NOS: 154
SOOTWARE: Patentin Ver. 2.0
SEQ ID NO 119
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Pred. No. 6.9e-88;
0; Mismatches 64; Indels 0;
                                                                                                                                                                                                                                                                                                                         Sequence 119, Application US/09322409
Patent No. 6471957
                                                                                                                                                                                                               CCAGCCCAGAAGTAA 435
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Best Local Similarity 85.3%;
Matches 371; Conservative (
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US-09-322-409-119
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US-09-322-409-119
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CURRENT FILING DATE: 1999-12-01
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Best Local Similarity 85.3
Matches 371; Conservative
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CORGANISM: Felis catus
US-09-451-527-121
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US-10-262-439-119
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            APPLICANT: Dreitz, Marthew J.
APPLICANT: Dreitz, Marthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANIBE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MCLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT FILING DATE: 1999-12-01
EARLIER FILING DATE: 1999-05-28
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 119
LENGTH: 444
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Sequence 121, Application US/09451527

Patent No. 6482403

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee

APPLICANT: Yang, Shumin

APPLICANT: Yang, Shumin

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-2-c2

CURRENT APPLICATION NUMBER: US/09/451,527
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Pred. No. 6.9e-88;
0; Mismatches 64;
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Best Local Similarity 85.3%;
Matches 371; Conservative (
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Yang, Shumin
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ORGANISM: Felis catus
                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (10)..(441)
US-09-451-527-119
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GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Dreiz, Matthew J.
APPLICANT: Dreiz, Matthew J.
APPLICANT: Dreiz, Matthew J.
APPLICANT: Dreiz, Matthew J.
APPLICANT: Wonderling, Ramani S.
ITILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/10/262, 439
CURRENT APPLICATION NUMBER: US/09/451,527
FRIOR APPLICATION NUMBER: US/09/451,527
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-52-28
PRIOR FILING DATE: 1998-65-29
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 119
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Pred. No. 6.9e-88;
EARLIER APPLICATION NUMBER: 09/322,409
BARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 121
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Patent No. 7026139
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Sequence 121, Application US/10262439

GENERAL INFORMATION:

APPLICANT: Stain, Gek-Kee

APPLICANT: Wang, Shumin

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REPERENCE: IM 2-C2

CURRENT APPLICATION NUMBER: US/10/262,439

CURRENT FILING DATE: 1999-12-01

PRIOR PILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/087,306

PRIOR FILING DATE: 1999-05-28

NUMBER OF SEQ ID NOS: 174

SOFFWARE: PATCHTON POS: 174

SOFFWARE: PATCHTON NUMBER: 0/087,306

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 174
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                                                                                                                                                                                                                                                    Query Match 76.5%; Score 332.6; DB 5; Length 444; Best Local Similarity 85.3%; Pred. No. 6.9e-88; Matches 371; Conservative 0; Mismatches 64; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGCCCAGAGTAA 435
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                              TYPE: DNA
ORGANISM: Felis catus
                                                                                                                   , NAME/KEY: CDS
; LOCATION: (10)..(441)
US-10-262-439-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-262-439-121/c
LENGTH: 444
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Sequence 10, Application US/08133979A
Patent No. 5589582
GENERAL INFORMATION:
APPLICANT: Havley, Robert J.
APPLICANT: Ponath, Paul D.
APPLICANT: Rosa, Margaret D.
APPLICANT: Schacter, Bernice Z.
TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines Theref
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITT: Rosaland
STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 AGTTCACCCAGCCTGGCACTCGGCCCTGGCAACACGCGGTGGATGCCATCAAGGAGGCCCTG 316
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                                                                                                        Gaps
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0
              Length 444;
Score 332.6; DB 5; Length
Pred. No. 6.9e-88;
0; Mismatches 64; Indels
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3R: 61750-79
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 18M PC Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,9°
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NAME: Herron. Charles J.
REGISTRATION NUMBER: 28 019
REFERENCE/DOCKET NUMBER: 6175
TELECHONNEY ICATION INFORMATION:
TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10:
         76.5%;
85.3%;
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Best Local Similarity 85.3
Matches 371; Conservative
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; Sequence 10, Application US/08451213
; Patent No. 5863528
; GENERAL INFORMATION:
    APPLICANT: Hawley, Robert J.
    APPLICANT: Ponath, Paul D.
    APPLICANT: Monroy, Rodney L.
    APPLICANT: Schacter, Bernice Z.
    TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porc.:
    TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porc.:
    TORRESPONDENCES: 24
    CORRESPONDENCES: 24
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart for STREET: 6 Becker Farm Road
    CITY: Roseland
    STATE: New Jersey
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 798;
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85.3%; Pred. No. 8.9e-88;
ive 0; Mismatches 64;
                                                                                                                                                     61750-139
                ATTORNEY/AGENT INFORMATION:
NAME: Herron, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 61750
TELECOMMUNICATION INFORMATION:
TELEPHAX: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 798 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
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Best Local Similarity 85.3
Matches 371; Conservative
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HYPOTHETICAL: NO
CLASSIFICATION:
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APPLICANT: Hawley, Robert J.
APPLICANT: Ponath, Paul D.
APPLICANT: Rosa, Margaret D.
APPLICANT: Schacter, Bernice Z.
TILE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines There
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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STREET: 6 Becker Farm Road
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Best Local Similarity 85.3%;
Matches 371; Conservative (
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                                LENGTH: 798 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLLGY: LINEAR
HYPOTHETICAL: NO
SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: 3.5 inc
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STATE: New Jersey
COUNTRY: USA
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US-08-133-979A-10
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TYPE: DNA
ORGANISM: Felis
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                                                                                                                                                                    LENGTH: 432
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US-10-209-507-9
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 332.6; DB 2; Length 798;
Pred. No. 8.9e-88;
0; Mismatches 64; Indels 0
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,213
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,979
FILING DATE: October 8, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                NAME: Herron, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 61750
TELECOMMUNICATION INPORMATION:
TELEFAX: 201-994-1700
INPORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGCCCAGAAGTAA 435
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.5%;
Best Local Similarity 85.3%;
Matches 371; Conservative
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Sequence 9, Application US/10209507

Batent No. 6914134
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Audonnet, et al.
TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT VITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT VITLE OF INTERIOR APPLICATION NUMBER: US/10/209,507
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/617,594
PRIOR APPLICATION NUMBER: 60/193,332
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-03-30 TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V? ö 120 420 420 360 360 TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTTTACAAA 240 241 cadedectraceseses descreareas cerchaseas et cadedeareares es canon 300 9 61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 361 AAAAATTTCAAAGGAATCTGAAGGATTTTTTTTAACATCCCCTTTGACTGCTGGAAA TACAAGCAGCACTGCCCCCCCCCCCTGGAAACTTCCTGTGCAACCCAGATGATCACCTTC 301 TACAAGCAGCACTGCCCCTTACTCCGGAAACGCCCTGTGAAACCCAGACTATCACCTTC AAAAGTTTCAAAAAGAACCTGAAGGATTTTTCTTTGAGATCCCGTTTGACTGCTGGAAG Gaps ö Length 432; Score 331.2; DB 3; Length Pred. No. 1.8e-87; 0; Mismatches 63; Indels ; IOCATION: (1)..(429) ; OTHER INFORMATION: coding sequence of 3R4 feline GM-CSF US-09-617-594A-9 PRIOR APPLICATION NUMBER: 60/193,332
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR PLING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-11
PRIOR FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 9 FILE REPERENCE: 454313-3151.1 CURRENT APPLICATION NUMBER: US/09/617,594A CURRENT FILING DATE: 2000-07-14 Query Match
Best Local Similarity 85.4%;
Matches 369; Conservative CCAGCCCAGAAG 432 CCAGTCAAGAAG 432

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61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
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85.1%; Pred. No. 2e-87;
tive 0; Mismatches 65; Indels
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Patent No. 6730512
GENERAL INFORMATION:
APPLICANT: Chang, Lung-Ji
TITLE OF INVENTION: Combination Immunogene Therapy
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/638,702
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPAX: (352) 375-8800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                          APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-848-760B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 435 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
             CURRENT APPLICATION DATA:
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Best Local Similarity 85.1
Matches 370; Conservative
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US-09-826-025-8
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TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
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CCATION: (1)..(429)

CTHER INFORMATION: coding sequence of 3R4 feline GM-CSF gene

US-10-209-607-9
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
ATTWARE: PatentIn Ralease #1.0, Version #1.30
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COUNTRY: United States of America
             APPLICATION NUMBER: France 00 01761
PRIOR APPLICATION NUMBER: France > PRIOR FILING DATE: 2000-02-11
PRIOR PRIOR PAPLICATION NUMBER: France 99 09-
PRIOR FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: A32
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Patent No. 6248721
GENERAL INFORMATION:
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Best Local Similarity 85.4%;
Matches 369; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Felis sp.
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                                                   COMPUTER: FLORDY disk
COMPUTER: THOUSY disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/826,025
FILING DATE: 04-Apr-2001
CLASSIFICATION CURRENCH
APPLICATION NUMBER: 08/838,702
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                NAME: Ingolia, Diane E.
REGIESTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CHANG-02687
TELECOMMUNICATION INFORMATION:
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 435 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                            COMPUTER READABLE FORM:
                            ZIP: 94104
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RESULT 15 US-09-543-679A-2706

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGGTGCCATGTGCATGCCATCAAGGAGGCCCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 cérticitéaactreagtagagacactgetgetgetgagatgaatgaaacatagaet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 CGCTCGCCCCAGCCCCAGCACGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                           APPLICANT: NYCE, JONATHAN W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF ALTRAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65; Indels
                                                                                                                                                                                                    ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.1%; Score 331; DB 5;
85.1%; Pred. No. 2.6e-87;
iive 0; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-APT-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION: UNKNOWN
FILING DATE: 1998-08-03
ATTORNEY AGENT INFORMATION:
NAME: AMZEL, Viviana
REGISTRATION WUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 2706
US-09-543-679A-2706
Sequence 2706, Application US/09543679A
Patent No. 7034007
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 2706:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  NUMBER OF SEQUENCES: 3111 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 85.1
Matches 370; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: N/A
                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                    STATE: NJ
                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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Search completed: May 26, 2006, 01:29:01 Job time : 166 secs

BEST AVAILABLE COPY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US08_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US09_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US09_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US09_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10F_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10F_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11B_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11B_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 119, App
Sequence 121, App
Sequence 119, App
Sequence 121, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Appli
Sequence 8, Appli
Sequence 14, Appl
Sequence 17, Appl
                                                                                                                               May 26, 2006, 01:24:10 ; Search time 1032 Seconds (without alignments) 5179.381 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                     1 atgiggotgcagaaccigct......ggaagccagcccagaagtaa 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1
Sequence 1
Sequence 1
Sequence 1
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-218 654-119
US-10-218 654-121
US-10-22-439-121
US-10-262-439-121
US-10-209-507-9
US-10-083-590-14
US-10-411-037-17
US-10-411-049-17
US-10-411-049-17
US-10-411-049-17
US-10-411-037-17
                                                                                                                                                                                                                                                                                                                                                                                                  18892170 segs, 6143817638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Applications NA Main: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                    US-10-614-481-8
                                                                                                                                                                                                                                                                                                                             IDENTITY_NUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published
                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332.6
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                                                                                        OM nucleic
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Maximum DB
                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
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	Seguence 8, Appli	Sequence 17, Appl	Sequence 17, Appl	7	Sequence 2, Appli	7	Sequence 16, Appl	0	Sequence 20, Appl	Sequence 16, Appl	Sequence 16, Appl	e 10	Sequence 10, Appl	ŝ	ń	122	Sequence 123, App	7, A	122,	123,	2, 7	32, 7	Sequence 15, Appl	16,	108,	109,	91, A	Sequence 82, Appl
-	US-10-785-\$77-8	US-10-410-980-17	.0 US-10-410-897-17	10 US-10-492-261-17	.1 US-10-937-658-2	.6 US-11-183-205-17	.6 US-11-201-384-16	3 US-10-609-346-19	3 US-10-447-315-20	7 US-10-131-985-16	US-10-901-417-16	.0 US-10-925-205-10	.5 US-11-066-480-10	10 US-10-925-205-5	.5 US-11-066-480-5	5 US-10-218-654-122	. US-10-218-654-123	. US-10-209-507-7	7 US-10-262-439-122	/ US-10-262-439-123	US-09-783-708-2	, US-10-188-056-32	US-10-775-204	10 US-10-775-204-16	10 US-10-775-204-108	.0 US-10-775-204-109	7 US-10-267-384-191	) US-10-688-845-82
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	43	43	43	43	435	43	43	448	781	78	789	900	8	117	1172	433	43	432	43	432	183	43	43	43	43	435	49	505
	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	75.8	75.8	75.8	75.8	75.8	75.8	75.7	75.7	75.7	75.7	75.7	75.7	75.7
	331	331	331	331	331	331	331	331	331	331	331	331	331	331	331	329.6	329.6	329.6	329.6	329.6	329.6	329.4	329.4	329.4	329.4	329.4	329.4	329.4
	18	19	20	21	22	23	24	25	56	27	28	5	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

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61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCATGTGGATGCCATCAAGGAGGCCCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CGCCAACCCAGCCCTGTCACTCGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1)..(432)
CTHER INFORMATION: coding sequence of equine GM-CSF gene US-10-614-481-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 435; DB 10;
100.0%; Pred. No. 8.7e-131;
cive 0; Mismatches 0;
US-10-614-481-8
Sequence 8, Application US/10614481
Sequence 8, Application US/10614481
Sequence 8, Application US/10614481
GENERAL INFORMATION:
APPLICANT: Bublot, et al.
TITLE OF INVENTION: Equine GM-CSF
FILE REFERENCE: 454313-2334.1
CURRENT APPLICATION NUMBER: US/10/614,481
CURRENT FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 1999-06-10
SPIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 9
SOCIETAL OF SEQ ID NOS: 9
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 435; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Equine sp.
                                                                                                                                                                                                                                                                                                                         LENGTH: 435
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Best Local S
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APPLICANT: Yang, Shumin
APPLICANT: Parg, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
ITILE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
ITILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
ITILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
ILLE REPERBUES: Mo. 2012 - 08 - 13
CURRENT APPLICATION NUMBER: US/10/218,654
CURRENT APPLICATION NUMBER: US/09/322,409
PRIOR PAPLICATION NUMBER: 60/087,306
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998 - 05 - 29
NUMBER OF SEQ ID NOS: 154
SSQ ID NOS: 154
SSQ ID NOS: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACAAGCAGCACCCCCCCCCCCCCCGGAAACTTCCTGTGCAACCCCAGATGATCACCTTC 360
                                                                                                                                                         435 Archdechechdeadchderrinnechdedechenderengeadchreneradaeden 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 AGTTCACCCAGCTCTGTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGGAGGCCCTG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGAAACGTTTGACGCCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAAGCTGTACAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 AAAAGTITCAAAAAGAACCIGAAGGAITITCCIGITTGAGATCCCGITTGACTGCTGGAAG 420
CAGGGCCTACGGGGCGCCTCATCAGCCTCTAAGGAGCCTCTGAGAATGATGGCCAACCAT 309
                                                                                                                                     361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACAAGCAGCACTGCCCCCTTACTCCGGAAAGGCCCTGTGAAACCCAGACTATCACTTC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAATTTCAAAGAGAATCTGAAGGATTTTTCTGTTTAACAACCCCTTTGACTGCTGGGGA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 TACAAGCAGCACTCTCTTACTCCGGAAAGGCCCTGTGAAACCCAGGAAACCAGACTATCACCTTC
                                                           TACAAGCACTGCCCCCCCCCCTGGAAACTTCCTGTGCAACCCAAGATGATCACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCATGTGGATGCCATCAAGGAGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.5%; Score 332.6; DB 6; Best Local Similarity 85.3%; Pred. No. 2.1e-97; Matches 371; Conservative 0; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                ; Sequence 121, Application US/10218654; Publication No. US20030099609A1; GENERAL INFORMATION: APPLICANT: Sim, Gek-Kee
                                                                                                                                                                                                               421 CCAGCCCAGAAGTAA 435
                                                                                                                                                                                                                                                     430 CCAGACCAGAAGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Felis catus US-10-218-654-121
                                                                                                                                                                                                                                                                                                                                US-10-218-654-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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APPLICANT: Yang, Shumin
APPLICANT: Yang, Shumin
APPLICANT: Wonderling, Ramani S.
ITLE OF INVENTION: CANINE AND FELINE IMMUNORECULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
CURRENT FILING DATE: 1090-08-13
PRIOR APPLICATION NUMBER: US/09/322,409
PRIOR FILING DATE: 1990-05-29
PRIOR FILING DATE: 1990-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PRICHIN VET. 2.0
SEQ ID NO 119
                                                                               240
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     69
                                                                 241 CAGGCCTTGCGGGGCAGCCTCATCAAGCTCGAAGGCCCCTTGACCATGATGGCCAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 119, Application US/10218654; Publication No. US20030099609A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            CCAGCCCAGAAGTAA 435
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Best Local Similarity 85.33
Matches 371; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (10)..(441)
US-10-218-654-119
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US-10-218-654-119
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APPLICANT: Yang, Shumin
APPLICANT: Yang, Shumin
APPLICANT: Wang, Shumin
APPLICANT: Wonderling, Ramani S.
ITILE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
ITILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
ITILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
ITILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
FRIOR FILING DATE: 1999-12-01
FRIOR APPLICATION NUMBER: US/09/451,527
FRIOR FILING DATE: 1999-12-01
FRIOR APPLICATION NUMBER: 60/087,306
FRIOR APPLICATION NUMBER: 60/087,306
FRIOR APPLICATION NUMBER: 60/087,306
FRIOR APPLICATION NUMBER: 60/087,306
FRIOR SEQ ID NOS: 114
SOFTWARE: PATENTING VOIC: 2.0
SEQ ID NO 121
LENGRARE: PATENTING VOIC: 2.0
SEQ ID NO 121
LENGRARE: ALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
76.5%; Score 332.6; DB 7
Best Local Similarity 85.3%; Pred. No. 2.1e-97;
Matches 371; Conservative 0; Mismatches 64
                                  Sequence 121, Application US/10262439
Publication No. US20030143196A1
GENERAL INFORMATION:
APPLICANT: Sim, Gek. Kee
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; ORGANISM: Felis catus
US-10-262-439-121
                     US-10-262-439-121/c
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US-10-209-507-9
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APPLICANT: Yang, Shumin
APPLICANT: Vang, Shumin
APPLICANT: Vang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
TITLE OF INVENTION NUMBER: US/10/262,439
CURRENT PILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCATGTGGATGCCATCAAGGAGGCCCTG 120
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                                                                                                                                        Sequence 119, Application US/10262439
Publication No. US20030143196A1
GENERAL INFORMATION:
421 CCAGCCCAGAAGTAA 435
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                            15 CCAGACCAGAAGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: CDS
; LOCATION: (10)..(441)
US-10-262-439-119
                                                                                                                       US-10-262-439-119
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Sequence 9, Application US/10209507
Publication No. US20030109033A1
GENERAL INFORMATION:
APPLICANT: Audonnet, et al.
TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT VI

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                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                       Length 432;
                                                                                                                                                                                                                                                    ; LOCATION: (1)...(429)
; OTHER INFORMATION: coding sequence of 3R4 feline GM-CSF gene US-10-209-507-9
                                                                                                                                                                                                                                                                                                                                  Indels
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Patent No. US20020162123A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Combination Immunogene Therapy
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                       Score 331.2; DB 6;
Pred. No. 6e-97;
0; Mismatches 63;
FILE REFERENCE: 454313-3151.2
CURRENT APPLICATION NUMBER: US/10/209,507
FURBENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/617,594
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-11
PRIOR PILING DATE: 2000-02-11
PRIOR PILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.4%;
Matches 369; Conservative (
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                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Felis sp.
                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                      LENGTH: 432
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                                                             COMPUTER READEDE FORM:

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
COSTWARE: PATCHIN PC-DOS/MS-DOS
COSTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/826,025
FILING DATE: 04-Apr-2001
CLASSIFICATION NUMBER: 08/838,702
FILING DATE: CUNKNOWN>
PRIOR APPLICATION NUMBER: 08/838,702
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: CHANG-02687
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.1%; Score 331; DB 3; Length 43
85.1%; Pred. No. 7e-97;
tive 0; Mismatches 65; Indels
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-826-025-8
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US-10-083-590-14
Sequence 14, Application US/10083590
; Publication No. US20030027257A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 435 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                          ZIP: 94104
COMPUTER READABLE FORM:
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Best Local Similarity 85.1
Matches 370; Conservative
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61 CGCTCGCCCAGCCCCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG 120
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Pred. No. 7e-97;
0; Mismatches 65; Indels
                  CURRENT APPLICATION NUMBER: US/10/411,037
CURRENT APPLICATION NUMBER: US/10/411,037
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-10-19
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 17
SEQ ID NO 17
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Publication No. US20040063911A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.1%;
Best Local Similarity 85.1%;
Matches 370; Conservative
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; ORGANISM: Homo sapiens
US-10-411-037-17
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Publication No. US20040043446A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Sopf. David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: APPLICANT: APPLICANT: Takes, David
APPLICANT: Tofen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
                          APPLICANT: IATROU, KOSTAS

APPLICANT: FARRELL, PARTICK J.
APPLICANT: BEHIE, Leo A.
TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF
TITLE OF INVENTION: NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS
TITLE OF INVENTION: NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS
TITLE OF INVENTION: NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS
CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/256,694
PRIOR FILING DATE: BARLIER PRILING DATE: 1999-02-24
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATCHTIN VET. 2.0
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Pred. No. 7e-97;
0; Mismatches 65; Indels
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85.1%;
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Best Local Similarity 85.1
Matches 370; Conservative
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-411-037-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 14
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85.1%; Pred. No. 7e-97;
ive 0; Mismatches 65; Indels
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US-10-411-049-17
Sequence 17, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
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Matches 370; Conservative
Bayer, Robert
Hakes, David
                        Hakes, David
Chen, Xi
Bowe, Caryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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               TITLE OF INVENTION: METHODS

TITLE OF INVENTION: METHODS

FILE REFERENCE: 0.0463-0.1-6.56

FILE REFERENCE: 0.0463-0.1-6.56

CURRENT APPLICATION NUMBER: US 60/328,523

FRIOR APPLICATION NUMBER: US 60/328,523

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR PRILING DATE: 2002-06-07

PRIOR PRILING DATE: 2002-06-15

PRIOR APPLICATION NUMBER: US 60/404,249

PRIOR APPLICATION NUMBER: US 60/404,249

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR PILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR PILING DATE: 2002-08-16
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Pred. No. 7e-97;
0; Mismatches 65; Indels
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Publication No. US20040077836A1
GENERAL INFORMATION:
APPLICANT: Noose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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Best Local Similarity 85.1%;
Matches 370; Conservative
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ORGANISM: Homo sapiens
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US-10-410-962-17
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GRERRAL INCOMENTION CONTROL CANDERS AND CAPPLICANT: Nocee Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Topf, David
APPLICANT: Topf, David
APPLICANT: Hakes, David
APPLICANT: David
APPLICANT: NUMBER: US 60/328,523
FRIOR FILING DATE: 2001-10-10
PRIOR PLING DATE: 2001-10-10
PRIOR PLING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR PLING DATE: 2002-09-17
PRIOR PLING DATE: 2002-09-17
PRIOR PLING DATE: 2002-09-17
PRIOR PLING DATE: 2002-09-17
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Best Local Similarity 85.1%; Pred. No. 7e-97;
Matches 370; Conservative 0; Mismatches 65; Indels
Application US/10410930
No. US20040115168A1
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CORGANISM: Homo sapiens
US-10-410-930-17
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                 APPLICANT: DeFree, Shawn
APPLICANT: DeFree, Shawn
APPLICANT: DeFree, Shawn
APPLICANT: DeFree, David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Bayer, Bayer
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERPERON
TITLE OF INVENTION: ALPHA
TITLE OF INVENTION: ALPHA
TITLE OF INVENTION: ALPHA
FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR PELLOR DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
CEPOTION NUMBER: PATENTIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.1%; Score 331; DB 8; Length 43 Best Local Similarity 85.1%; Pred. No. 7e-97; Matches 370; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccacrccaggagga 435
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US-10-410-930-17
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APPLICANT: Defrees, Shawn
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APPLICANT: Zoyf, David
APPLICANT: Zoyf, David
APPLICANT: Active Robert
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryne
APPLICANT: Bowe, Caryne
APPLICANT: Bowe, Caryne
APPLICANT: Bowe, Caryne
TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: WEBER: US 60/328,523
PRIOR PELICATION NUMBER: US 60/387,292
PRIOR PELING DATE: 2001-10-19
PRIOR PELING DATE: 2002-06-25
PRIOR PELING DATE: 2002-06-25
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-16
PRIOR PELING DATE: 2002-06-16
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Pred. No. 7e-97;
0; Mismatches 65; Indels
                                                                                                                                                                                           Sequence 17, Application US/10411012
Publication No. US20040132640A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.1%;
Matches 370; Conservative C
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-012-17
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APPLICANT: DeFrees, Shawn
APPLICANT: DoFrees, Shawn
APPLICANT: DoFrees, Shawn
APPLICANT: DoFrees, Shawn
APPLICANT: DoFrees, David
APPLICANT: APPLICANT: Chen, Xi
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Bayer, Nobert
APPLICANT: Bayer, Saryn
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: US 60/326,523
FILE REFRENCE: 02001-0-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-06-07
PRIOR PELICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PELING DATE: 2002-00-17
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR PELING DATE: 2002-08-16
PRIOR PERIOR PELING DATE: 2002-08-16
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                                                                                               Sequence 17, Application US/10410997
Publication No. US20040126838A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PutentIn version 3.2
SEQ ID NO 17
LENGTH: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-410-997-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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Search completed: May 26, 2006, 01:41:32 Job time : 1034 secs

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Query Match
Best Local S:
Matches 144
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Sequence 11, Appl
Sequence 11, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 11, Appl
Sequence 11, Appl
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Sequence 11, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 12, Appli
Sequence 120, Appl
Sequence 120, Appl
Sequence 120, Appl
Sequence 120, Appl
Sequence 120, Appl
Sequence 120, Appl
Sequence 10, Appl
Sequence 11, Appli
                                                                                                      (without alignments)
252.088 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
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            GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                        May 25, 2006, 15:01:08 ; Search time 50 Seconds
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US-08-133-979A-11
US-08-4316-8911
US-08-431-8911
US-08-212-217-114
US-09-522-217-114
US-10-295-213-216-114
US-10-295-622-10
US-10-295-622-10
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US-09-55-165-9
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US-09-617-594A-10
US-09-617-594A-10
US-09-617-594A-10
US-09-617-594A-10
US-09-507-8
US-08-295-696B-9
US-08-295-696B-10
US-08-259-696B-10
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                               Scoring table:
                                                                                                                                                         Perfect score:
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                                                               OM protein
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No.
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NGS-08-133-979A-11
Sequence 11, Application US/08133979A
Sequence 11, Application US/08133979A
Patent No. 5589582
GENERAL INFORMATION:
APPLICANT: Hawley, Robert J.
APPLICANT: Rosa, Margaret D.
APPLICANT: Monroy, Rodney L.
APPLICANT: Benice Z.
TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines Theref
NUMBER OF SEQUENCES: 24
                                                                                                          Sequence 142, App
Sequence 142, App
Sequence 142, App
Sequence 142, App
Sequence 2, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 160, App
Sequence 160, App
Sequence 160, App
                         Sequence 10, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Patent No. 5405952
Patent No. 5229496
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Patent No.
Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 75%; DB 2;
100.0%; Pred. No. 1.7e-82;
tive 0; Mismatches 0;
                                                                                             5229496-2
US-08-468-609A-142
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US-08-762-227A-142
PCT-US95-01185-142
US-08-318-193-2
US-09-462-941-8
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US-08-468-609A-160
US-08-446-872A-160
                         US-08-318-193-10
US-09-146-283-4
US-08-579-823A-4
US-09-344-195-4
5405952-2
                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09589460
| Patent No. 6645740
| GENERAL INFORMATION:
| APPLICANT BUBLOL, et al.
| TILLE OF INVENTION: Equine GM-CSF
| FILE REPERENCE: 454313-2334.1
| CURRENT APPLICATION NUMBER: US/09/589,460
| CURRENT FILING DATE: 2000-06-07
| PRIOR APPLICATION NUMBER: 60/138,843
| PRIOR FILING DATE: 1999-06-10
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                               5229496-15
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  ; LENGTH: 144
; TYPE: PRT
; ORGANISM: Equine sp
US-09-589-460-9
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Sequence 11, Application US/08451213
Fatent No. 5863528
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hawley, Robert J.
APPLICANT: Rosa, Margaret D.
APPLICANT: Rosa, Margaret D.
APPLICANT: Schacter, Bernice Z.
TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines Therei
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.3%; Score 587; DB 1; Best Local Similarity 76.4%; Pred. No. 5.7e-62; Matches 110; Conservative 13; Mismatches 21;
          CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,890
FILING DATE: MAY 8, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Herron, Charles U-
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 61750-139
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,213
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/133,979
FILING DATE: OCCODER 8, 1993
ATTORNEY/AGENT INFORMATION:
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|21 KSFKDSLNKFLFTIPFDCWGPVKK 144
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                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: SINGLE TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE: NO
US-08-436-890-11
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APPLICANT: Hawley, Robert J.
APPLICANT: Rosa, Margaret D.
APPLICANT: Rosa, Margaret D.
APPLICANT: Schacter, Bernice Z.
TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines There
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SETFDAEELICLOTRLKLYKOGLRGSLIKLEGPLIMMASHYKOHCPPTLETSCATOMITF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CEMFDPQEPTCVQTRLNLYKQGLRGSLTRLKSPLTLLAKHYEQHCPLTEETSCETQSITF 120
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        ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,Stewart & Olstein STREET: 6 Becker Farm Road CITY: Roseland STATE: New Jersey COUNTRY: USA ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein STREET: 6 Becker Farm Road CITY: Roseland STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MWLQNLLLLGTVVCSISAPTRPPSPVTRPWQHVDAIKEALSLLNNSNDTAAVMNETVDVV
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                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 138 PC Compatible
COMPUTER: 158 PC Compatible
COMPUTER: 158 PC Compatible
COMPUTER: 158 PC Compatible
COMPUTER: 158 PC COMPATION
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/13,979A
FILING DATE: October 8, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Herron, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 61750-79
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KSFKKNLKDFLFEIPFDCWKPAQK 144
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08436890
Patent No. 5858963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 144 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 76.4%
Matches 110; Conservative
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LINEAR
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CORRESPONDENCE ADDRESS:
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HYPOTHETICAL:
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US-08-133-979A-11
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US-08-436-890-11
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61 SEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTWMASHYKQHCPPTPETSCATQIITF 120
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                                                                1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                        0; Gaps
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Best Local Similarity 76.4%; Pred. No. 7.5e-62;
Matches 110; Conservative 15; Mismatches 19; Indels
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CURRENT FILING DATE: 2000-03-09
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-01
SARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOSTWARE: FRELSEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.2%; Score 586; DB 2; Lv 76.4%; Pred. No. 7.5e-62; iive 15; Mismatches 19;
                                                                                                                                                                                                                                      121 KSFKKNLKDFLFEIPFDCWKPAQK 144
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GENERAL INFORMATION:
APPLICANT: No. 6605272ak, Julia E.
APPLICANT: Presnell, Scott R.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 114, Application US/09522217 Patent No. 6307024
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: No. 6307024ak, Julia E
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Matches 110, Conservative
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ORGANISM: Homo sapiens
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US-09-522-217-114
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,393B
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08284393B
Patent No. 5696234
GENERAL INFORMATION:
APPLICANT: Zurawski, Sandra M.
APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
NUMBER OF SEQUENCES: 16
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSFKKNLKDFLFEIPFDCWKPAQK 144
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                    TELECOMMUNICATION INFORMATION:
TELEPANE: 201-994-1740
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 AMINO ACIDS
TYPE: AMINO ACID
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NAME: Ching, Edwin P.
RECISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
  REFERENCE/DOCKET NUMBER:
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amino acid
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Matches 110; Conservative
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LINEAR
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STATE: California
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-282-622-10
                     TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-723-114
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US-10-282-622-10
LENGTH: 144
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APPLICANT: Foster, Donald C.
APPLICANT: Gross, Jane A.
APPLICANT: Gross, Jane A.
APPLICANT: Gross, Jane A.
APPLICANT: Gross, Jane A.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND
FILE REPERBNCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
FRIOR PAPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
FRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
FRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/142,013
FRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
FRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/142,013
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APPLICANT: Poster, Donald C.
APPLICANT: Gester, Donald C.
APPLICANT: Golder A.
APPLICANT: Golder A.
APPLICANT: Johnston, Jane A.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dellon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: BILLON Stacey R.
APPLICANT: BILLON STACES 109/10/295,723
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT PILLING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FasteSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.2%; Score 586; DB 2; 76.4%; Pred. No. 7.5e-62;
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; Sequence 114, Application US/10295723
; Patent No. 6686178
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APPLICANT: No. 6686178ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
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Best Local Similarity 76.4%
Matches 110; Conservative
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Sprecher,
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                         1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
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    Length 144;
                                                 19; Indels
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PCT-US95-08950-11
; Sequence 11, Application PC/TUS9508950
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCALATION:

APPLICANT: Presnell, Scott R.

APPLICANT: West, James W.

APPLICANT: West, James W.

APPLICANT: No. 6929332ak, Julia E.

TILLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS;
FILE REFRENCE: 01-37

CURRENT APPLICATION NUMBER: US/10/282, 622

CURRENT FILING DATE: 2001-11-05

PRIOR FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 144
; Score 586; DB 2;
; Pred. No. 7.5e-62;
15; Mismatches 19
                                                                                                                                                                                                                                                                                                        121 KSFKKNLKDFLFEIPFDCWKPAQK 144
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; Patent No. 6929932
    77.2%;
    Query Match
Best Local Similarity 76.4
Matches 110; Conservative
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0; Gaps

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61 SETFDAEELTCLOTRLKLYKOGLRGSLIKLEGPLTMMASHYKOHCPPTLETSCATOMITF 120
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                                                                                                                                                                       1 MWLQNLLLLGTVVYSMPAPTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVV
                                                                                                                                                                                                   1 MWLQSLLLLGTVACSISAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Artifically synthesized human GM-CSF-human mpl; OTHER INFORMATION: fusion protein sequence US-09-555-165-11
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Patent No. 6225446
GENERAL INFORMATION:
APPLICANT: APPLICANT: Rock, Fernando L.
APPLICANT: Razan, J. Fernando L.
APPLICANT: Kastelain, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
                                                                        Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 334;
                                                                     Query Match 77.2%; Score 586; DB 2; Length 33 Best Local Similarity 76.4%; Pred. No. 2.6e-61; Matches 110; Conservative 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.2%; Score 586; DB 2; Length 33 76.4%; Pred. No. 2.6e-61; ive 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KOJIMA, TETSUO
TITLE OF INVENTION: SIGNAL SEQUENCE TRAPPING METHOD
FILE REFERENCE: 06510-061001
CURRENT APPLICATION NUMBER: US/09/555,165
CURRENT FILING DATE: 2000-05-28
PRIOR APPLICATION NUMBER: JP 9/324912
PRIOR FILING DATE: 1999-11-26
PRIOR FILING DATE: 1999-11-26
PRIOR FILING DATE: 1999-11-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1: 15
LENGTH: 334
OTHER INFORMATION: fusion protein sequence
                                                                                                                                                                                                                                                                                                                                                                        121 KSFKKNLKDFLFEIPFDCWKPAOK 144
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Patent No. 6866998
GENERAL INFORMATION:
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Best Local Similarity 76.4
Matches 110; Conservative
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       ; OTHER INFURN
US-09-555-165-9
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US-08-759-628-6
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OTHER INFORMATION: Artifically synthesized human GM-CSF-human mpl
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APPLICANT: Kitamura, Toshio
TITLE OF INVENTION: SIGNAL SEQUENCE TRAPPING METHOD
FILE REFERENCE: 06501-061001
CURRENT APPLICATION NUMBER: US/09/555,165
CURRENT FILING DATE: 2000-05-28
PRIOR APPLICATION NUMBER: D9/324912
PRIOR APPLICATION NUMBER: PCT/JP98/05326
PRIOR PLING DATE: 1999-11-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: RateRef for Windows Version 4.0
SEQ ID NO 9
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 586; DB 5;
Pred. No. 7.5e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches
                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDABR:
ILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-852-9196
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Patent No. 6866998
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 77.2%;
Best Local Similarity 76.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
California
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                                              94304-1104
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                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-08950-11
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Gaps

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GENERAL INFORMATION:
APPLICANT: AUGOMOTE, et al.
TITLE OP INVENTION: FELLIE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V;
FILE REFERENCE: 454313-3151.2
CURRENT APPLICATION NUMBER: US/10/209,507
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/617,594
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: France 00 01761
PRIOR PILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PALENTH VERSION 3.0
SEQ ID NO 10
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                                                                                                                                                                            Length 143;
                                                                                                                                                                            76.2%; Score 578; DB 2; Length 14:
76.9%; Pred. No. 6.7e-61;
cive 9; Mismatches 24; Indels
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Job time : 51 secs
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Patent No. 6914134
                SOFTWARE: Patentin version 3.0
SEQ ID NO 10
LENGTH: 143
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Matches 110; Conservative
                                                                                                                                                                                                                          Matches 110; Conservative
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                      ; TYPE: PRT
; ORGANISM: Felis sp.
US-09-617-594A-10
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ORGANISM: Felis sp.
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APPLICANT: Audonnet, et al.
TITLE OF INVENTION: FELLINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT 1TILE DOF INVENTION: FELLINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT 1TILE REFERENCE: 454313-3151.1
CURRENT APPLICATION NUMBER: US/09/617,594A
CURRENT FILING DATE: 2000-07-14
PRIOR PELLING DATE: 2000-03-30
PRIOR PLILING DATE: 2000-03-30
PRIOR PLILING DATE: 2000-03-11
PRIOR PLILING DATE: 1999-07-16
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                                                                                                                                                                                                                                                         SOFTWARE: Patentn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/759,628 FILING DATE: 05-DEC-1996 CLASSIFICATION: 435
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OTHER INFORMATION: /note= "peptide of Figure 1"
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                                                                                                                                                                                                                                                                                                                                                                                    PRICA APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTATION NUMBER: 34,090
REPERRICE/DOCKET NUMBER: DX0552Q
TELECOMMUNICATION INFORMATION:
                                           ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSFKKNLKDFLFEIPFDCWKPAQK 144
                                                                                                                                                       ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 10, Application US/09617594A
; Patent No. 6541458
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415-852-9196
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amino acid
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Matches 110; Conservative
NUMBER OF SEQUENCES: 11
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                     CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                      CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
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                                                                                                                                                                                                          (without alignments)
376.853 Million cell updates/sec
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/BMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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1 MWLQNLLLLGTVVYSMPAPT......KNLKDFLFBIPFDCWKPAQK 144
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                                                                                                                                                                     May 25, 2006, 15:12:58; Search time 177 Seconds
GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-923-246-114

US-10-285-523-114

US-10-131-985-15

US-10-131-985-15

US-10-131-985-15

US-10-131-985-15

US-10-411-037-18

US-10-411-026-18

US-10-447-315-19

US-10-447-315-19

US-10-447-915-18

US-10-441-095-18

US-10-411-012-18

US-10-411-012-18

US-10-411-012-18

US-10-411-012-18

US-10-411-012-18

US-10-411-012-18

US-10-659-295-27

US-10-66-122-3

US-10-668-84-83

US-10-610-918-114
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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61 SETFDAEELTCLQTRLKLYKQGLRGSLIKUEGPLTMMASHYKQHCPPTLETSCATQMITF 120
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118, Appl
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100.0%; Pred. No. 3.1e-78;
iive 0; Mismatches 0;
US-10-410-897-18
US-10-892-261-18
US-10-775-204-44-7
US-10-775-204-44-8
US-10-775-204-44-8
US-10-775-204-54-0
US-11-175-204-54-0
US-11-175-204-54-0
US-11-183-205-18
US-10-775-204-32-4
US-10-775-204-32-4
US-10-775-204-32-4
US-10-351-157-181
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US-10-937-658-3
US-11-066-480-6
US-11-201-384-14
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Publication No. US20606059121A1
GENERAL INFORMATION: 64 al.
TITLE OF INVENTION: Equine GM-CSF
FILE REFERENCE: 454313-2334.1
CURRENT FILING DATE: 2003-07-07
PRIOR APPLICATION NUMBER: US/09/589,460
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
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US-09-923-246-114
Sequence 114, Application US/09923246
Fatent No. US20020128446A1
GENERAL INFORMATION:
APPLICANT: No. US20020128446A1ak, Julia E.
APPLICANT: Pesnell, Scott R.
APPLICANT: Foster, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
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Best Local Similarity 100.
Matches 144; Conservative
     ; TYPE: PRT
; ORGANISM: Equine
US-10-614-481-9
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APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey W.
APPLICANT: Hamond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT FILING DATE: 2001-08-03
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/522,217
PRIOR PELLING DATE: EARLIER FILING DATE: 2000-03-09
FRIOR PILING DATE: EARLIER FILING DATE: 1999-03-11
FRIOR PILING DATE: EARLIER FILING DATE: 1999-03-11
FRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
FRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
SOFTWARE: FASTSEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
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APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND
FILE REFERENCE: 99-16
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PRIOR APPLICATION NUMBER: 09/522,217

PRIOR FILING DATE: 2000-00-09

PRIOR FILING DATE: 1999-03-09

PRIOR FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: US 60/123,904

PRIOR APPLICATION NUMBER: US 60/123,904

PRIOR APPLICATION NUMBER: US 60/142,013

PRIOR PILING DATE: 1999-07-01

NUMBER: OF SEQ ID NOS: 115

SOCTWARE: FastSEQ for Windows Version 3.0

LENGTH: 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/295,723 CURRENT FILING DATE: 2002-11-15
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, Sequence 114, Application US/10295723
, Publication No. US20030125524A1
Johnston, Janet V.
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Best Local Similarity 76.4*
Matches 110; Conservative
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ORGANISM: Homo sapiens
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US-09-923-246-114
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77.2%; Score 586; DB 4; Length 144; 76.4%; Pred. No. 1.8e-58; Live 15; Mismatches 19; Indels
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APPLICANT: West, James W.
APPLICANT: No. US20030134390Alak, Julia E.
TITLE OF INVENTION: ZALFHAll LIGAND ANTAGONISTS
FILE REPERENCE: 01-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 144
TYPE: PRI
ORGANISM: Homo sapiens
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APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
APPLICANT: Fish, Paul V
APPLICANT: McIntosh, Fraser S
APPLICANT: Occleston, Nicholas I
TITLE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT FILING DATE: 2002-04-25
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                                                                                                                                                                                                                                                                                121 KSFKKNLKDFLFEIPFDCWKPAQK 144
                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 10, Application US/10282622; Publication No. US20030134390A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 15, Application US/10131985; Publication No. US20030199440A1
  Query Match
Best Local Similarity 76.49
Matches 110; Conservative
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Best Local Similarity 76.4
Matches 110; Conservative
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US-10-282-622-10
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GABERAL INCRAMYION:

APPLICANT: Neces Technologies, Inc.

APPLICANT: Sof, David

APPLICANT: Sof, David

APPLICANT: Sof, David

APPLICANT: Toof, David

APPLICANT: Hakes, David

APPLICANT: Bowe, Caryn

TITLE OF INVENTION: ALPHA GLACTOSIDASE A: REWODELING AND GLYCCCONJUGATION OF ALPHA

TITLE OF INVENTION: GLACTOSIDASE A

FILE REFREENCE: 04083-101-508

CURRENT APPLICANTON NUMBER: US 60/328,523

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR PRIOR OF SEQ ID NOS: 75

SOFTWARE: PATENTIN OF SEQ ID NOS: 75

SOFTWARE: PATENTIN OF SEQ ID NOS: 75

SOFTWARE: PATENTIN OF SEQ ID NOS: 75

SEMICANT: LANGTH: 144
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                      APPLICANT: Hughes, Steven D.
APPLICANT: Hughes, Steven D.
APPLICANT: Hughes, Steven D.
APPLICANT: Hughes, Steven D.
TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
FILE REFERENCE: 03-08
CURRENT APPLICATION NUMBER: US/10/456,780
CURRENT FILING DATE: 2003-06-06
PRIOR FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 144
TYPE: PRT
TYPE: PRT
TYPE: RT
CORANISM: Homo sapiens
US-10-456-780-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/10411037; Publication No. US20040043446A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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; Sequence 217, Application US/10116275
; Publication No. US20030211476A1
; Publication No. US20030211476A1
; Publication No. US20030211476A1
; Publicant: O'Mahony, Daniel J.
APPLICANT: Blan Pharmaceutical Technology
; APPLICANT: Daniel J.
APPLICANT: Lambkin, Imeda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; TITLE OF INVENTION: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 144
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77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: GB 9930768.8
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-985-15
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Best Local Similarity 76.4%
Matches 110; Conservative
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US-10-116-275-217
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61 SETFDAEELTCLGTRLKLYKQGLRGSLIKLEGPLTWMASHYKQHCPPTLETSCATQMITF 120
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APPLICANT: Hattori, Koichi
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Adult Stem Cell Recruitment
FILE REFERENCE: 1676.006USI
CURRENT APPLICATION NUMBER: US/10/447,315
CURRENT APPLICATION NUMBER: US 60/383,658
PRIOR FILING DATE: 2002-05-28
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 18
LENGTH: 144
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 144
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GENERAL INFORMATION: APPLICANT: Rafii, Shahin
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Matches 110; Conservative
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US-10-447-315-19
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ORGANISM: Homo sapiens
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Publication No. US20040063911A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHODS
FILE OF INVENTION: WETHODS
FILE REPERENCE: 040853-01-5053
CURRENT APPLICATION NUMBER: US/10/411,026
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                                            77.2%; Score 586; DB 4; Length 144; 76.4%; Pred. No. 1.8e-58;
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Matches 110; Conservative
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ORGANISM: Homo sapiens
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, ORGANISM: Homo sapiens
US-10-411-049-18
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Sopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
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APPLICANT: Chen, Xi
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                                                                    121 KSFKKNLKDFLFEIPFDCWKPAQK 144
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Publication No. US20040082026A1
GENERAL INFORMATION:
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Publication No. US20040077836A1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-18
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| TITLE OF INVENTION: INTERFERENCY ALPHA: ERROBEING AND GIYCCCONJUGATION OF INTERFERENCY
TITLE OF INVENTION: LABOR
TITLE OF INVENTION: LABOR
TITLE OF INVENTION: ALPHA
TITLE STEERING OF INVENTION: ALPHA
TITLE STEERING AFFEL AND ALPHA
THE STEERING OF INVENTION: ALPHA
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THE APPLICATION NUMBER: US 60/40,237
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THE APPLICATION NUMB
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61 SEMPDLOEPTCLOTRLELYKQGLRGSLTKLKGPLTWMASHYKQHCPPTPETSCATQIITF 120
                                                                                                     121 KSFKKNLKDFLFEIPFDCWKPAQK 144
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APPLICANT: HAKER, DAVIG
APPLICANT: HAKER, DAVIG
APPLICANT: CHEN, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: DETA
FILE REFERENCE: 040853-01-5056
CURRENT PELLON HOMBER: US 60/328,523
PRIOR PELLON DATE: 2001-10-19
PRIOR PLING DATE: 2001-10-19
PRIOR PLING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR PAPLICATION NUMBER: US 60/391,777
PRIOR PALICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-06-25
PRIOR PAPLICATION NUMBER: US 60/404,249
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
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    NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 114
LENGTH: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KSFKKNLKDFLFEIPFDCWKPAQK 144 :|||:|||||||||||11 ESFKENLKDFLLVIPFDCWEPVQE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/10410930 Publication No. US20040115168A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Neose Technologies,
APPLICANT: DeFrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-930-18
                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-659-684-114
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US-10-410-930-18
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Sequence 2460, Ap
Sequence 18, Appl
Sequence 7275, Ap
Sequence 7273, Ap
Sequence 20993, A
Sequence 13150, A
Sequence 15150, A
Sequence 18543, A
Sequence 18541, A
Sequence 18541, A
Sequence 13760, A
Sequence 24953, A
Sequence 20916, A
Sequence 266, Appl
Sequence 266, Appl
Sequence 266, A
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                                                                                                                   (without alignments)
114.555 Million cell updates/sec
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Sequence 8, App
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/ EMC_Celerra_SIDS3/prodata/2/pubpaa/US06_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/2/pubpaa/US06_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_NEW_PUB.pep:*
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/ EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_NEW_PUB.pep:*
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1 MWLQNLLLLGTVVYSMPAPT......KNLKDFLFEIPPDCWKPAQK 144
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                May 25, 2006, 15:13:17; Search time 14 Seconds
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US-11-183-218-18

US-10-953-349-7275

US-10-953-349-7273

US-10-953-349-7273

US-10-953-349-7273

US-10-953-349-20993

US-10-953-349-18542

US-10-953-349-18542

US-10-953-349-13761

US-10-953-349-13761

US-10-953-349-13761

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US-10-953-349-20915

US-10-953-349-20916

US-10-953-349-20916

US-10-953-349-10265

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US-10-953-349-10265

US-10-953-349-10265
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Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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seq length: 200000000
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Match Length
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Perfect score:
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Maximum DB
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                                                                                                  Run on:
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No.
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Sequence 851, App	Sequence 850, App	Sequence 849, App	Sequence 20021, A	Sequence 3373, Ap	Sequence 4624, Ap	Sequence 4318, Ap	Sequence 22, Appl	Sequence 24, Appl	Sequence 26, Appl	Sequence 46, Appl	Sequence 2709, Ap	Seguence 13506, A	Sequence 18, Appl	Sequence 18874, A	Sequence 15286, A	Sequence 2214, Ap	Sequence 2213, Ap	539, A	Sequence 537, App
US-10-953-349-851	US-10-953-349-850	US-10-953-349-849	US-10-953-349-20021	US-11-293-697-3373	US-11-293-697-4624	US-11-293-697-4318	US-11-181-115-22	US-11-181-115-24	US-11-181-115-26	US-11-181-115-46	US-11-293-697-2709	US-10-953-349-13506	US-11-314-018-18	US-10-953-349-18874	US-10-953-349-15286	US-10-953-349-2214	US-10-953-349-2213	US-10-505-928-539	US-10-505-928-537
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319	336	342	352	361	392	611	664	664	664	664	142	362	1332	377	177	332	346	201	1193
8.3	8.3	8.3	8.3	8.3	8.3	8.3	8.2	8.2	8.2	8.2	8.2	8.2	8.2	8.1	8.0	8.0	8.0	8.0	8.0
63	63	63	63	63	63	63	62.5	62.5	62.5	62.5	62	62	62	61.5	61	61	61	60.5	60.5
36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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61 SETFDAEELICLOTRLKLYKQGLRGSLIKLEGPLTWMASHYKQHCPPTLETSCATQMITF 120
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                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Modward, Robert
APPLICANT: Morris, MacDonald
APPLICANT: Prontice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND NONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 506012000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT PILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
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Sequence 2460, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
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Best Local Similarity 76.4
Matches 110, Conservative
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US-10-511-937-2460
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CURRENT APPLICATION NUMBER: US/10/953,349
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                       CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7274
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; ORGANISM: Arabidopsis thaliana
US-10-953-349-7273
                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7275
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Matches 28; Conserv
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SETFDABELICLOTRIKLYKOGLRGSLIKLEGPLIMMASHYKOHCPPILETSCATOMITF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITF 120
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: HAKES, DAVIG
APPLICANT: HAKES, DAVIG
APPLICANT: HAKES, DAVIG
APPLICANT: HAKES, LAVIG
APPLICANT: HOWE, Caryne
TITLE OF INVENTION: EXPTHROPOLETIN: REMODELING AND
TITLE OF INVENTION: EXPTHROPOLETIN
FILE REFERENCE: 040853-01-5083-0205-07-15
CURRENT APPLICATION NUMBER: US/11/183,218
CURRENT PELING DATE: 2005-04-09
PRIOR PILING DATE: 2002-04-09
PRIOR PLING DATE: 2002-06-28
PRIOR PLING DATE: 2002-08-28
PRIOR PLING DATE: 2002-08-28
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-11-28
PRIOR PLING DATE: 2001-11-128
PRIOR PLING DATE: 2001-11-19
PRIOR PLING DATE: 2001-11-19
PRIOR PLING DATE: 2001-11-10
PRIOR PLING DATE: 2001-11-10
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Pred. No. 5.2e-53;
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                                                 US-11-183-218-18
Sequence 18, Application US/11183218
Publication No. US20060088906A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.2%;
76.4%;
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US-11-183-218-18
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Best Local Similarity
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US-10-953-349-7275
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Sequence 7273, Application US/10953349
Fublication No. US20060107345A1
GENERAL INFORMATION:
FUBLICANT: ALEXANDROW, Nickolai et al.
TTPLICANT: ALEXANDROW, Nickolai et al.
TTPLICANT: ALEXANDROW, Nickolai et al.
TTPLICANT: ALEXANDROM: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 7273
LENGTH: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: BROOMDED THERBY
FILE OF INVENTION: BROOMDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 2274
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                                                                                                                                  34 DAIKEALSLLNNSS-----DTAAIMNETVEVVSE--TFDAEELTCLQTRLKLYKQG-LR 84
                                                                                                                                                                                                                                                          85 GSLIKLEGPLTMMASHYKQHCPPTLETSCATQM-----ITFKSFKKNLKDFLFEIP 135
                                                                                                                                                                                                                                                                                               133 NAETKYSGVIDCITKVPRSEGIPGLYRGCATNLLRTTPSAVITFTTYEMMLRFFRQVVP 191
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                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Gaps
10.0%; Score 76; DB 6; Length 243; 23.5%; Pred. No. 0.89; tive 26; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.0%; Score 76; DB 6; Length 285; Best Local Similarity 23.5%; Pred. No. 1.1; Matches 28; Conservative 26; Mismatches 43; Indels
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US-10-953-349-15150
US-10-953-349-15150
Sequence 15150, Application US/10953349
Sequence 15150, Application US/10953349
Sequence 15150, Application US-10953349
Sequence 15150, Application No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US,10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 15150
LENGTH: 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LVLLGLNLMVTAVHGGCGPHCPTPTPPPPPSTNGGSCSIDTLKLRVCANVLNLLKLGLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 EALSLINNSSDIAAIMNETVEVVSETFDAEELTCLQTRLKLYKQGLRGSLIKLEGPLTMM
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85 GSLIKLEGPLTMMASHYKOHCPPTLETSCÅTOMITFKSFKKNLKDFLFEIPFDCWK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 734;
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                                      223 NIVTKAVSLLKQEKLSKKAHCPRLLPPPSAIEDVR-KSLKINKQQFL
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25.8%; Pred. No. 2.3;
tive 17; Mismatches 49;
                                                                                                                                                                     Sequence 3300, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length CDNA
FILE REPERENCE: H.-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR PAPLICATION NUMBER: US/10/108,260
PRIOR FULING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 3300
LENGTH: 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.3%; Score 70.5; D
Best Local Similarity 28.7%; Pred. No. 13;
Matches 31; Conservative 13; Mismatches
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Matches 31; Conservative
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CORGANISM: Homo sapiens
US-11-293-697-3300
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US-10-953-349-18543
                                                                                                                              RESULT 8
US-11-293-697-3300
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICAMY: ALEXANDROV, Nickolai et al.
APPLICAMY: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALENTIN Version 3.3
SEQ ID NO 20992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579-90432
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
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EKIKQYMAKMDNTSVENLSPGNVAIASSIAKVIASILITYPHEVI-----RAKLQEĞGQIR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 VLPPYQHKGYGRFLLEVLYDVAISENVFDFTVEEPLDHFQRVR-TCVDA-LRLLRFGPIQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 VLPPYQHKGYGRPLLEVLYDVAISENVFDFTVEEPLDHFQRVR-TCVDA-LRLLRFGPIQ 222
                                                                                                                                    84
                                                                                                                                                                                                                                                                     253 NAETKYSGVIDCIIKVFRSEGIPGLYRGCATNLLRITPSAVITFTTYEMMLRFFRQVVP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 VTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVVSETFDAEELTCLQTRLKLYKQG-LR 84
                                                                                                                                                                                                                                       85 GSLIKLEGPLTMMASHYKQHCPPTLETSCATQM-----ITFKSFKKNLKDFLFEIP 135
                                                                                                                                 34 DAIKEALSLINNSS-----DTAAIMNETVEVVSE--TFDAEELTCLQTRLKLYKQG-LR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 VTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVVSETFDAEELTCLQTRLKLYKQG-LR
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                           10.0%; Score 76; DB 6; Length 363; 23.5%; Pred. No. 1.5; ive 26; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 71.5; DB 26.7%; Pred. No. 3.2; tive 19; Mismatches
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Publication No. US20060107345A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.7%
Matches 31; Conservative
                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Glycine max US-10-953-349-20993
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Best Local Similarity
Matches 31; Conserv
                           Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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LENGTH: 293
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 18541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24953, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
GERREAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 24953
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 NNSNNDAFMRNQNAAVQARTKAQNRSNVLQLKLIGQSHPTGLTANLLKLFEPRPPLEYKP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 NNSSDTAAIMNETVEVVSETFDAEELTCLQTRL--KLYKQGLRGSLIKL---EGPLTMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 SSPAPTKKPL----WOHLSEBALLAKLDPSVAWSYRRALSSRNLGRNTLSRDVRSMGSS
                                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.0%; Score 68.5; DB 6; Length 482; 30.4%; Pred. No. 12; Live 11; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                              DB 6; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                            40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TFKSFKKÅLKDFL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 PLIFHSSFSFGKNNSLCRLSGTEDRIVLYCTSLRG--
                                                                                                                                                                                                                                                                                                                                            Query Match 9.0%; Score 68.5; D
Best Local Similarity 22.4%; Pred. No. 11;
Matches 35; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       15 SMPAPTRQPSPVTRPWQHVD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 SHYKQHCPP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 PPEKRKCPP 72
                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Glycine max
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Matches 21; Conserv
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US-10-953-349-24953
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GRNERAL INFORMATION:
TITLE OF INVENTION: BEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
SOFTWARE: Patentin Version 3.3
SEQ ID NOS: 40252
SOFTWARE: Patentin Version 3.3
                GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickclai et al.
TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTI VERSION 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 SSPAPTKKPL----WQHLSEEALLAKLDPSVAWSYRRALSSRNLGRNTLSRDVRSMGSS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 TVEVVSETFDAEE-----LTCLQTRLKLYKQGLRGSLIKLEGPLTMMASHYKQHCPPTL 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AIKEALSLLN-----NSSDTAAIMNE
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 364;
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                                                                                                                                                                                                                                                                                                                                                                                                                    40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ETSCATQMI------TFKSFKKNLKDFL 131
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22.4%; Pred. No. 8.6;
tive 18; Mismatches
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Publication No. US20060107345A1
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Best Local Similarity 22.44
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                , ORGANISM: Glycine max US-10-953-349-18543
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US-10-953-349-18542
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                                                                                                                                                                                                                               SEQ ID NO 18543
                                                                                                                                                                                                                                                       LENGTH: 364
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RESULT 15
US-10-953-149-13760
US-10-953-149-13760
Sequence 13760, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVEXTION: ENCONDED THERBY
TITLE OF INVEXTION: ENCONDED THERBY
TITLE OF INVEXTION: ENCONDED THERBY
TITLE OF INVEXTION: ENCONDED THERBY
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTION OF 13760
LENGTH: 445
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                                                                                                                                                                                                                                                                                                                                                                                       183 SSVAASLVQDTVTLATDPVPAYTFGCIQKATGSSLPPQGLLG---LGRGPLSLLAQTQKL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 SSDTAAIMWETVEVVSETFDAEELTCLQ--TRLKLYKQGLRGSLIKLEGPLTMMASHYK- 102
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8.9%; Score 67.5; DB 6; Length 442;
Best Local Similarity 29.7%; Pred. No. 14;
Matches 22; Conservative 14; Mismatches 27; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Indels 11; Gaps
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 13761
LENGTH: 442
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240 YQSTFSYCLPSFKT 253
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                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13761
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; ORGANISM: Glycine max
US-10-953-349-13760
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Search completed: May 25, 2006, 15:16:25 Job time : 14 secs

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